MycoKeys 113: 209–236 (2025)
DOI: 10.3897/mycokeys.113.140684

Research Article

Freshwater fungi in the karst plateau wetlands from Guizhou Province, China: taxonomic novelties in Melanommataceae (Pleosporales)

Ling-Ling Liu[1,2], Yong-Xiang Liu[2], Ya-Ya Chen[2,3], Jiu-Lan Gou[1], Feng Chi[4], Yi Liu[5], Xiao-Feng Gu[1], Quan-Quan Wei[1], Meng Zhang[1], Zuo-Yi Liu[2], Si Zhou[4]

1 *Guizhou Provincial Institute of Soil and Fertilizer, Guizhou Academy of Agricultural Sciences, Guiyang, China*
2 *Guizhou Key Laboratory of Agricultural Biotechnology, Guizhou Academy of Agricultural Sciences, Guiyang, China*
3 *Guizhou Provincial Institute of Crop Germplasm Resources, Guizhou Academy of Agricultural Sciences, Guiyang, China*
4 *Guizhou Provincial Environmental Science Research and Design Institute, Guiyang, China*
5 *Guizhou Caohai National Nature Reserve Management Committee, Bijie, China*
Corresponding author: Si Zhou (sparklingenergy@163.com)

Abstract

Three isolates of interest were collected during an investigation of freshwater fungi from wetlands in the karst regions of Guizhou Province, Southwest China. Phylogenetic analyses using ITS, LSU, SSU, and *tef-1α* gene regions have revealed the placements of these isolates in Melanommataceae (Pleosporales, Dothideomycetes). Based on the morphological and phylogenetic evidence, three new species are introduced: *Byssosphaeria chishuiensis* **sp. nov.**, *Camposporium guizhouense* **sp. nov.**, and *C. aquaticum* **sp. nov.** *Byssosphaeria chishuiensis* is sister to *B. villosa* and forms a basal branch of *Byssosphaeria* within Melanommataceae. *Byssosphaeria chishuiense* is similar to *B. villosa* in ascal size but differs in the ascomata and ascospore sizes, and the ascospores lack appendages. *Camposporium aquaticum* is sister to *C. guizhouense*, and they form a distinct lineage within the genus. Morphologically, *C. aquaticum* resembles *C. guizhouense* in its conidial shape but differs in conidial size. Additionally, PHI analysis is performed to further reveal that *C. aquaticum* and *C. guizhouense* have no significant recombination with related taxa. *Neobyssosphaeria* is synonymized under *Byssosphaeria*, and accordingly, *Byssosphaeria clematidis* **comb. nov.** is proposed to accommodate *Neobyssosphaeria clematidis*. The descriptions, illustrations, and notes of the novel taxa are provided along with an updated phylogenetic tree of Melanommataceae. Two synopses of the species in *Byssosphaeria* and *Camposporium* are also provided.

Key words: Aquatic fungi, ascomycota, four new taxa, generic delimitation, molecular phylogeny

OPEN ACCESS

Academic editor:
Chitrabhanu S. Bhunjun
Received: 31 October 2024
Accepted: 27 December 2024
Published: 7 February 2025

Citation: Liu L-L, Liu Y-X, Chen Y-Y, Gou J-L, Chi F, Liu Y, Gu X-F, Wei Q-Q, Zhang M, Liu Z-Y, Zhou S (2025) Freshwater fungi in the karst plateau wetlands from Guizhou Province, China: taxonomic novelties in Melanommataceae (Pleosporales). MycoKeys 113: 209–236. https://doi.org/10.3897/mycokeys.113.140684

Copyright: © Ling-Ling Liu et al.
This is an open access article distributed under terms of the Creative Commons Attribution License (Attribution 4.0 International – CC BY 4.0).

Introduction

The family Melanommataceae was introduced by Winter (1885) with *Melanomma* as the type genus. Melanommataceae members are characterized by globose or depressed perithecial ascomata, trabeculate pseudoparaphyses, bitunicate and fissitunicate asci, and pigmented and phragmosporous

ascospores (Sivanesan 1984; Barr 1990; Zhang et al. 2012; Hyde et al. 2013; Tian et al. 2015; Li et al. 2017; Tennakoon et al. 2018). The trabeculate pseudoparaphyses is an important identification character of this family (Liew et al. 2000; Zhang et al. 2012; Hyde et al. 2013; Tian et al. 2015; Li et al. 2017; Tibpromma et al. 2017). Most species in this family have diverse lifestyles and habitats. They are fungicolous, hyperparasitic, parasitic, or saprobic and occur mainly on the twigs or bark of various woody plants in terrestrial, marine, and freshwater habitats in temperate and subtropical regions (Zhang et al. 2012; Hyde et al. 2013; Tian et al. 2015; Hashimoto et al. 2017; Wijayawardene et al. 2017; Beenken et al. 2020; Hongsanan et al. 2020). Mycologists have recently studied this family extensively (Mugambi and Huhndorf 2009; Hyde et al. 2013; Wijayawardene et al. 2014a, 2014b, 2017, 2020, 2022; Liu et al. 2015; Tian et al. 2015; Hyde et al. 2016; Tennakoon et al. 2018; Tibpromma et al. 2018; Beenken et al. 2020; Hongsanan et al. 2020; Bánki et al. 2023). Tian et al. (2015) reviewed Melanommataceae and accepted 20 genera in this family, including 13 sexual and 7 asexual genera. Subsequently, four genera, *Marjia*, *Melanocucurbitaria*, *Monoseptella*, and *Uzbekistanica*, were introduced by Wanasinghe et al. (2018a) based on the morphological and phylogenetic analyses. Koukol and Delgado (2021) reduced *Fusiconidium* and *Pseudobyssosphaeria* to synonymy with *Camposporium* and *Bertiella*, respectively. Recently, Gao et al. (2023) introduced *Dematiomelanomma*, resulting in 35 accepted genera in Melanommataceae, of which 28 genera have available sequence data (Koukol and Delgado 2021; Wijayawardene et al. 2022; Gao et al. 2023).

Byssosphaeria was introduced by Cooke and Plowright (1879) and typified by *B. keithii*. However, cultures and sequences of the type species are unavailable. *Byssosphaeria* spp. are characterized by superficial, separate, or gregarious ascomata, with a minute rounded ostiole and a coelomycetous asexual morph (Barr 1990; Hawksworth et al. 1995; Tennakoon et al. 2018). Asexual morphs have been reported in sporulated cultures as chaetophoma-like (Barr 1984) or pyrenochaeta-like coelomycetes (Samuels and Müller 1978). *Byssosphaeria* spp. are widespread, particularly on decorticated wood, bark of fallen branches, old leaves, and other plant substrates (Kirk et al. 2001; Zhang et al. 2012; Hyde et al. 2013; Tian et al. 2015; Tennakoon et al. 2018; Wanasinghe et al. 2018b; Kularathnage et al. 2022). Tennakoon et al. (2018) reviewed this genus and described two *Byssosphaeria* species (*B. macarangae* and *B. taiwanense*) in Melanommataceae based on multigene phylogenetic analyses. Index Fungorum (July 2024) listed 19 species. However, only 12 species have available sequence data (Tennakoon et al. 2018; Kularathnage et al. 2022).

Camposporium was introduced by Harkness (1884) and is typified by *C. antennatum*. The genus is polymorphic (Koukol and Delgado 2021) and characterized by dematiaceous, simple conidiophores and terminal, integrated, conidiogenous cells; the conidia are typically cylindrical and elongate, multi-septate, and rounded at one or both ends; the cells at each end are often paler in pigmentation than the central cells; the apex is either simple or has one or more cylindrical appendages; and the base typically has a persistent portion of the denticle attached (Hughes 1951; Ellis 1971; Ichinoe 1971; Whitton et al. 2002; Dong et al. 2020). Species of this cosmopolitan genus have been reported from

freshwater and terrestrial habitats in many countries (Argentina, Australia, Brunei, Canada, China, Hawaii, Hungary, India, Japan, and Thailand) (Rao and Rao 1964; Dudka 1966; Ichinoe 1971; Matsushima 1971, 1983; Shearer 1974; Ellis 1976; Abdullah 1980; Castañeda 1985; Mercado et al. 1995; Whitton et al. 2002; Hyde et al. 2020a).

Most *Camposporium* spp. have cylindrical conidia with one or more appendages, and few have fusiform conidia, for example, *C. fusisporum* (Whitton et al. 2002), whereas others lack appendages (such as *C. ontariense* and *C. indicum*), which is reminiscent of those of *Fusiconidium* species. In a recent study, *Fusiconidium* was synonymized under *Camposporium* by Koukol and Delgado (2021) based on morphological comparisons (Koukol and Delgado 2021) and multigene phylogenetic analyses (Hyde et al. 2020a; Calabon et al. 2021). Twenty-five species epithets are listed in Index Fungorum (July 2024). However, sequence data are available for only 11 species.

During a survey of the taxonomy and diversity of freshwater fungi from karst plateau wetlands in Guizhou Province, China (Liu et al. 2019, 2020, 2023a, 2023b, 2023c; Yang et al. 2021, 2023), fresh collections were obtained from submerged decaying wood in freshwater and identified based on morphological and phylogenetic analyses. We introduce four novel species, *Byssosphaeria chishuiense* sp. nov., *B. clematidis* comb. nov., *Camposporium aquaticum* sp. nov., and *C. guizhouense* sp. nov., with an illustrated account and molecular evidence. Their phylogenetic positions were determined based on maximum likelihood and Bayesian inference of combined ITS, LSU, SSU, and *tef-1α* sequence data.

Materials and methods

Specimen collection and examination

Specimens of submerged, decaying twigs were collected from wetlands in Guizhou Province, China, taken to the laboratory in zip-lock plastic bags, and incubated in plastic boxes lined with moistened, sterile filter paper at room temperature for one week. The Motic Nikon SMZ-171 (Nikon, Tokyo, Japan) dissecting microscope was used to observe fungal colonies and fruiting bodies. Fungal structures were examined and photographed using a Nikon ECLIPSE 80i compound microscope (Nikon) fitted with a Canon 70D digital camera (Canon, Tokyo, Japan). Single spores were isolated on water agar (**WA**), and germinated spores were transferred on potato dextrose agar (**PDA**) as described by Luo et al. (2018) and Senanayake et al. (2020). The Tarosoft Image Framework program was used for measurement, and the images used for photo plates were processed using Adobe Photoshop CS6 software. Herbarium specimens were deposited in the herbarium of the Guizhou Academy of Agriculture Sciences (**GZAAS**), Guiyang, China, and the herbarium of Cryptogams, Kunming Institute of Botany Academia Sinica (**HKAS**), Kunming, China. Axenic cultures were deposited to the Agricultural Culture Collection of China (**ACCC**) or Guizhou Culture Collection (**GZCC**). Facesoffungi and Index Fungorum numbers were registered as outlined by Jayasiri et al. (2015) and Index Fungorum (2024).

DNA extraction, PCR amplification, and sequencing

Fungal mycelia were scraped using a sterilized scalpel and transferred to a 1.5 mL microcentrifuge tube for genomic DNA extraction with an Ezup Column Fungi Genomic DNA Purification Kit (Sangon Biotech, China). DNA was amplified by polymerase chain reaction (PCR). The ITS, LSU, SSU, and *tef-1α* gene regions were amplified using the primer pairs ITS5/ITS4 (White et al. 1990), LR0R/LR5 (Vilgalys and Hester 1990; Rehner and Samuels 1994), NS1/NS4 (White et al. 1990), and ef1-983F/ef1-2218R (Rehner and Buckley 2005), respectively, in a 25 µL reaction volume containing 9.5 µL ddH_2O, 12.5 µL 2 × Taq PCR Master Mix with blue dye (Sangon Biotech, China), 1 µL of DNA template, and 1 µL of each primer (10 µM). The amplification condition consisted of initial denaturation at 94 °C for 3 min, followed by 40 cycles of 45 s at 94 °C, 50 s at 56 °C, and 1 min at 72 °C, and a final extension period at 72 °C for 10 min. The PCR products were purified and sequenced by Shanghai Sangon Biological Engineering Technology and Services Co. (Shanghai, China).

Alignments and phylogenetic analyses

The ex-type and additional strains of Melanommataceae members were selected for phylogenetic analyses. The reverse and forward sequences generated in this study were assembled using DNAstar-SeqMan and subjected to BLASTn searches in the GenBank nucleotide database (http://blast.ncbi.nlm.nih.gov/, accessed on 12 May, 2024) to determine the most probable closely related taxa. The sequences were aligned using the online multiple alignment program MAFFT v.7 (http://mafft.cbrc.jp/alignment/server/, accessed on 12 May, 2024; Katoh and Standley 2013) and edited manually using BioEdit 7.2.3 (Hall 1999). The uninformative gaps and ambiguous regions were removed by trimAL v1.2 (http://trimal.cgenomics.org, accessed on 12 May, 2024; Capella-Gutiérrez et al. 2009) and manually combined in SequenceMatrix (Vaidya et al. 2011). The FASTA files were transferred to PHYLIP (for ML) and NEXUS (for BI) formats using the Alignment (ALTER) online program (Glez-Peña et al. 2010). Maximum likelihood (ML) analyses were performed on the CIPRES Science Gateway V. 3.3 (Miller et al. 2010). ML analyses were conducted with the RAxML-HPC v. 8.2.12 tool (Stamatakis 2014) using a GTRGAMMA approximation with rapid bootstrap analysis followed by 1000 bootstrap replicates. For the Bayesian inference (BI) approach, MrModeltest2 v. 2.3 (Nylander et al. 2008) was used to infer the appropriate substitution models. The GTR+G+I substitution model was selected for ITS, LSU, SSU, and *tef-1α* partitions. BI analyses were performed with MrBayes 3.2.6 (Ronquist et al. 2012). Six simultaneous Markov chains were run until the average standard deviation of the split frequencies was < 0.01, with trees saved every 1000 generations. The first 25% of saved trees, representing the burn-in phase, were discarded. The remaining trees were used to calculate the posterior probabilities (PP) of the recovered branches (Larget and Simon 1999).

The resulting trees were printed using FigTree v. 1.4.0 (Rambaut 2012), and the layout was edited using Adobe Illustrator 2019. The sequences generated in this study have been deposited in GenBank (Table 1).

Table 1. Taxa used in the phylogenetic analyses and their GenBank accession numbers. T denotes ex-type strains. Newly generated sequences and combined novel species are indicated in bold.

Taxon	Culture Accession No.	GenBank Culture Accession No.			
		ITS	LSU	SSU	*Tef-1α*
Alpinaria rhododendri	CBS 141994^{T}	KY189973	KY189973	KY190004	KY190009
Aposphaeria corallinolutea	MFLU 15–2752	KY554202	KY554197	KY554200	KY554205
Aposphaeria corallinolutea	MFLUCC 14–0504	–	KU243051	KU243052	KU243050
Bertiella bambusae	MFLUCC 18–0145^{T}	MG737556	MG737555	–	MG737557
Bertiella ellipsoidea	MFLU 16–0583^{T}	KX765261	KX765262	–	KX765263
Bertiella fici	NCYU 19–0073^{T}	–	MW063224	MW079352	MW183787
Bertiella macrospora	IL 5005^{T}	–	GU385150	–	–
Bertiella macrospora	SMH 3953^{T}	–	–	–	GU327744
Beverwykella pulmonaria	CBS 283.53	KY189974	KY189974	KY190005	–
Byssosphaeria chishuiense	**ACCC 35242^{T}**	**PQ164697**	**MW133847**	**MW134626**	**PQ231192**
Byssosphaeria clematidis	**MFLUCC 17–0794^{T}**	**–**	**MT214566**	**MT408594**	**–**
Byssosphaeria diffusa	CBS 250.62^{T}	–	DQ678071	DQ678019	DQ677915
Byssosphaeria guangdongense	ZHKUCC 22–0335	OQ449320	OQ449288	OQ449337	–
Byssosphaeria guangdongense	ZHKUCC 22–0336	OQ449321	OQ449289	OQ449338	–
Byssosphaeria jamaicana	SMH 1403^{T}	–	GU385152	–	GU327746
Byssosphaeria macarangae	MFLUCC 17–2655^{T}	MH389782	MH389778	MH389780	MH389784
Byssosphaeria musae	MFLUCC 11–0146^{T}	KP744435	KP744477	KP753947	MH581149
Byssosphaeria rhodomphala	GKM L153N^{T}	–	GU385157	–	GU327747
Byssosphaeria salebrosa	SMH 2387^{T}	–	GU385162	–	GU327748
Byssosphaeria schiedermayeriana	GKM 152N^{T}	–	GU385168	–	GU327749
Byssosphaeria siamensis	MFLUCC 10–0099^{T}	–	KT289895	KT289897	KT962059
Byssosphaeria taiwanense	MFLUCC17–2643^{T}	MH389783	MH389779	MH389781	MH389785
Byssosphaeria villosa	GKM 204N	–	GU385151	–	GU327751
Camposporium appendiculata	DLUCC 1234^{T}	MN758890	MN759021	MN758956	MN784094
Camposporium aquaticum	**ACCC 35528^{T}**	**PQ164699**	**MW133849**	**MW134628**	**PQ231194**
Camposporium atypicum	NFCCI 4039	MF588672	MF588673	–	–
Camposporium cambrense	FMR 12069	KY853428	KY853488	HF937343	–
Camposporium guizhouense	**GZCC19–0480^{T}**	**PQ164698**	**MW133848**	**MW134627**	**PQ231193**
Camposporium dulciaquae	MFLUCC 21–0009^{T}	MT864352	MT860430	MW485612	MW537104
Camposporium lycopodiellae	CBS 143437^{T}	MH107892	MH107939	–	–
Camposporium multiseptata	DLUCC 792^{T}	MN758889	MN759020	MN758955	MN784093
Camposporium pellucidum	DLUCC 1239	MN758891	MN759022	MN758957	MN784095
Camposporium septatum	MFLUCC 19–0483^{T}	NR168243	MN759023	NG068424	MN784096
Camposporium ramosum	CBS 132483	MH866030	MH877478	HF937344	–
Camposporium valdivianum	MFLUCC 14–0434^{T}	–	KX611112	KX611114	KX611118
Camposporium verruculosum	MFLUCC 16-0991^{T}	–	KX641894	–	KX641896
Cyclothyriella rubronotata	CBS 121892^{T}	KX650541	KX650541	–	KX650516
Cyclothyriella rubronotata	CBS 141486	KX650544	KX650544	KX650507	KX650519
Dematiomelanomma yunnanense	KUNCC 23–12728^{T}	OQ225528	OQ360647	OQ360651	OQ413238
Dematiomelanomma yunnanense	KUNCC 23–12730	OQ225529	OQ360648	OQ360652	OQ413239
Herpotrichia juniperi	CBS 200.31^{T}	–	DQ678080	DQ678029	DQ677925
Herpotrichia macrotricha	SMH 269	–	GU385177	–	GU327756
Herpotrichia xiaokongense	KUMCC 21–0004^{T}	–	MZ408889	MZ408891	MZ394066
Herpotrichia vaginatispora	MFLUCC 13–0865^{T}	–	KT934252	KT934256	KT934260
Marjia tianschanica	TASM 6120^{T}	MG828909	MG829019	MG829126	MG829206
Marjia uzbekistanica	TASM 6122^{T}	MG828911	MG829021	MG829128	MG829208
Melanocamarosporioides ugamica	MFLUCC 17–2314^{T}	MH000192	MH000190	MH000191	MH006610
Melanocucurbitaria uzbekistanica	MFLUCC 17–0829^{T}	MG828912	MG829022	MG829129	MG829209

Taxon	Culture Accession No.	GenBank Culture Accession No.			
		ITS	LSU	SSU	*Tef-1α*
Melanodiplodia tianschanica	TASM 6111^{T}	MG828914	MG829023	MG829130	MG829210
Melanodiplodia tianschanica	MFLUCC 17–0805^{T}	MG828913	MG829025	MG829132	MG829212
Melanomma japonicum	CBS 142905^{T}	–	LC203338	LC203292	LC203367
Melanomma populicola	CBS 543.70	NR170056	NG075164	NG070237	–
Melanomma pulvis pyrius	CBS 124080^{T}	–	GU456323	GU456302	GU456265
Monoseptella rosae	MFLUCC 17–0815^{T}	MG828916	MG829026	MG829133	MG829213
Monoseptella rosae	TASM 6114	MG828917	MG829027	MG829134	MG829214
Muriformistrickeria rosae	MFLU 16–0227^{T}	MG828918	MG829028	MG829135	MG829215
Muriformistrickeria rubi	MFLUCC 17–2550	MG828919	MG829029	MG829136	MG829216
Muriformistrickeria rubi	MFLUCC 15–0681^{T}	–	KT934253	KT934257	KT934261
Petrakia echinata	WU 36922	KY189980	KY189980	KY190007	KY190015
Petrakia echinata	CBS 133070	JQ691628	LC203352	LC203306	LC203380
Phragmocephala atra	MFLUCC 15–0021^{T}	KP698721	KP698725	KP698729	–
Phragmocephala garethjonesii	MFLUCC 15–0018^{T}	KP698722	KP698726	KP698730	–
Phragmotrichum chailletii	CPC 33263^{T}	MN313812	MN317293	–	–
Pleotrichocladium opacum	AU BD04	JN995638	JN941370	JN938733	–
Pleotrichocladium opacum	FMR 12416^{T}	KY853462	KY853523	–	–
Praetumpfia obducens	WU 36895	KY189982	KY189982	–	KY190017
Praetumpfia obducens	CBS 141474^{T}	KY189984	KY189984	KY190008	KY190019
Pseudostrickeria muriformis	MFLUCC13–0764^{T}	–	KT934254	KT934258	KT934262
Pseudostrickeria ononidis	MFLUCC14–0949^{T}	–	KT934255	KT934259	KT934263
Pseudostrickeria rosae	MFLUCC 17–0643^{T}	MG828954	MG829065	MG829169	MG829234
Pseudotrichia mutabilis	WU 36923	KY189988	KY189988	–	KY190022
Pseudotrichia mutabilis	SMH 1541	–	GU385209	–	–
Sarimanas pseudofluviatile	MAFF 239465^{T}	LC001717	LC001714	LC001711	–
Sarimanas shirakamiense	HHUF 30454^{T}	NR138017	NG059803	NG061263	–
Seifertia azalea	ZTMyc 59953^{T}	MK502003	MK502026	MK502037	MK502083
Seifertia shangrilaensis	MFLUCC 16–0238^{T}	–	KU954100	KU954101	KU954102
Tumularia aquatica	CBS 212.46^{T}	MH856165	MH867689	–	–
Tumularia tuberculata	CBS 256.84	–	GU301851	–	GU349006
Uzbekistanica pruni	MFLU 17–2136^{T}	MN758893	MN759024		MN784097
Uzbekistanica rosae hissaricae	MFLUCC 17–0819^{T}	MG828975	MG829087	MG829187	MG829242
Uzbekistanica yakutkhanika	MFLUCC 17–0842^{T}	MG828978	MG829090	MG829190	MG829245
Xenostigmina zilleri	CBS 115685	GU269840	GU253857	–	–

Results

Phylogenetic analyses

The phylogenetic analyses of Melanommataceae isolates using combined ITS, LSU, SSU, and *tef-1α* sequences showed the three new strains represented three distinct lineages in the *Byssosphaeria* and *Camposporium* subclades (Fig. 1). The alignment comprised 84 strains with 3194 nucleotides (1–437, 438–1274, 1275–2274, and 2275–3194 bp of ITS, LSU, SSU, and *tef-1α*, respectively), including gaps. *Cyclothyriella rubronotata* (CBS 121892 and CBS 141486) served as the outgroup taxa. The best-scoring RAxML tree is shown in Fig. 1. The analyzed ML and Bayesian trees were topologically similar and did not conflict significantly.

The phylogenetic analyses of Melanommataceae showed that *Byssosphaeria* species clustered together to form a monophyletic subclade without significant support. The new isolate ACCC 35242 was sister to *B. villosa*

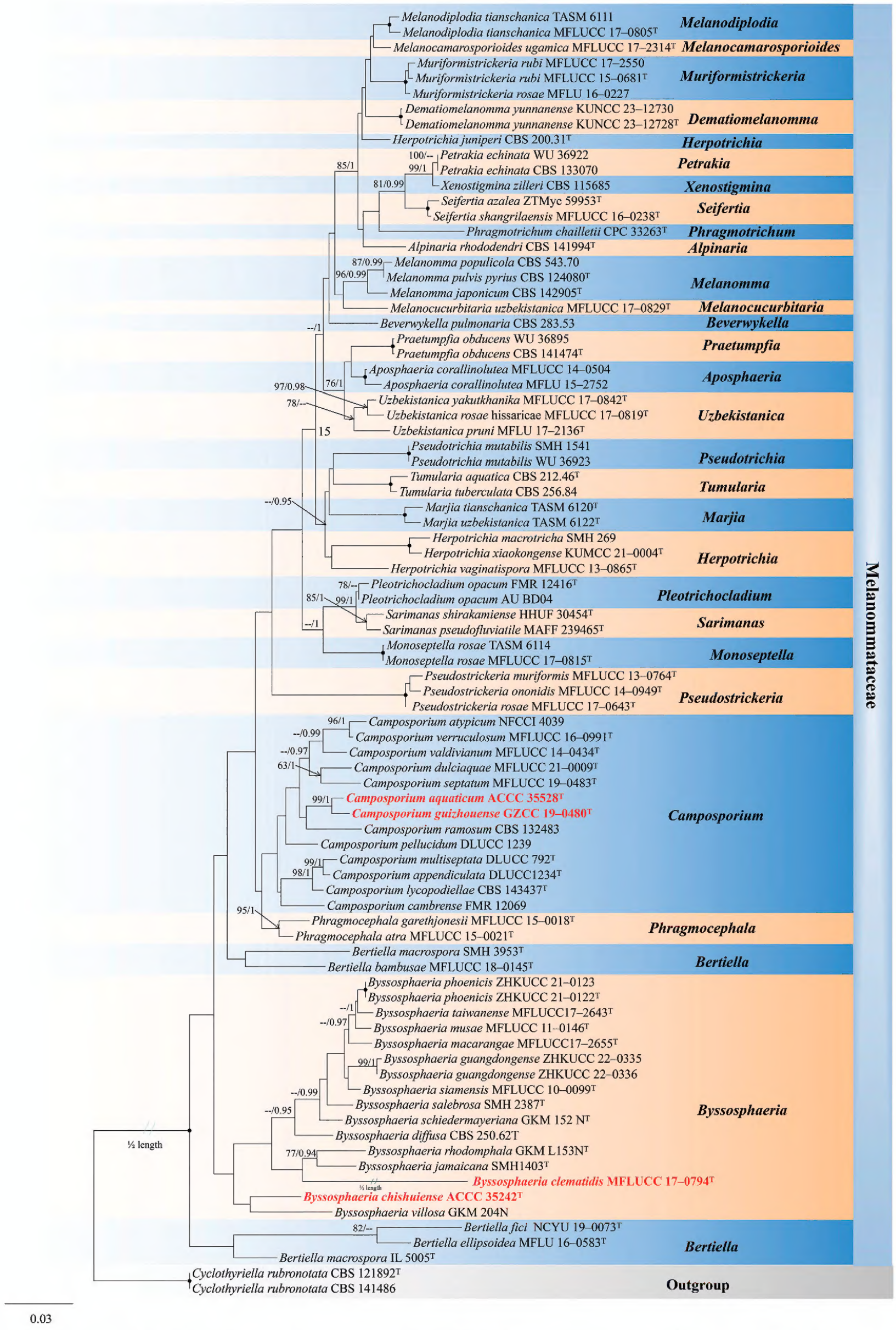

Figure 1. Maximum likelihood majority rule consensus tree for Melanommataceae using ITS, LSU, SSU, and *tef1-α* sequence data. Bootstrap support values for maximum likelihood (ML) greater than 75% and Bayesian posterior probabilities greater than 0.95 are indicated above branches as ML-BS/PP. The scale bar represents the expected number of changes per site. The tree is rooted with *Cyclothyriella rubronotata* (CBS 121892^{T} and CBS 141486). Ex-type strains are indicated with a superscript^{T}. The new taxa are in red and bold. Branches with 100% ML-BS and 1.0 PP were dotted with black dots. Genera are indicated as colored blocks.

(GKM 204N) with weak support. The two new isolates, GZCC19-0480 and ACCC 35528, clustered together within *Camposporium* with strong statistical support (99% ML BS/1.00 PP; Fig. 1) and were sister to *Camposporium ramosum* (CBS 132483) with weak support.

Taxonomy

***Byssosphaeria chishuiense* L.L. Liu & Z.Y. Liu, sp. nov.**
Index Fungorum: IF902545
Facesoffungi Number: FoF15497
Fig. 2

Etymology. Refers to the Chishui River basin, where the holotype was collected.

Holotype. GZAAS 20-0374.

Description. ***Saprobic*** on decaying, submerged wood in freshwater habitats. ***Sexual morph*. *Ascomata*** superficial, gregarious, unilocular, globose to subglobose, 220–390 µm high, 520–740 µm diam., broadly or narrowly conical, black, carbonaceous, roughened and irregular, ostiolate. ***Ostiole*** single, central, papillate. ***Peridium*** 33–58 µm wide at sides, brown, thick-walled, of ***textura angularis***, comprising a mixture of host and fungal cells. ***Hamathecium*** 2.5–3.5 µm wide, composed of dense, trabeculate, distinctly septate, anastomosing, pseudoparaphyses, embedded in a hyaline gelatinous matrix. ***Asci*** 111–163(–220) × 14–24.5 µm ($\bar{x}$ = 145 × 19 µm, n = 20), 8-spored, bitunicate, fissitunicate, cylindrical clavate, short pedicel, apically round, with an ocular chamber. ***Ascospores*** overlapping, 1–2-seriate, fusiform, hyaline, 1-septate, constricted at the central septum, lower cell wider and longer than upper cell, 41.5–51.5 × 7–9 µm ($\bar{x}$ = 45.5 × 8 µm, n = 30), tapering to pointed apices, mostly straight, surrounded by a thick distinctive sheath, 4–6.3 µm wide (in water-mounted slide), drawn out at the ends, smooth-walled. ***Asexual morph*.** Undetermined.

Cultural characteristics. Conidia germinated on WA, and germ tubes were produced from both ends within 12 h. Colonies on PDA overgrew the culture dish after 3 weeks at 25 °C in dark, circular, mycelia dense in the middle and sparse in the edge, white from above, pale yellow from reverse.

Material examined. China • Guizhou Province, Chishui River basin, near 28°25'N, 106°0'E, at 500 m altitude, saprobic on submerged decaying wood in a freshwater stream, July 2019, L.L. Liu, CS1-13 (GZAAS 20-0374, holotype); • ex-type living culture ACCC 35242.

Taxonomic notes. Morphologically, *B. chishuiense* is characterized by superficial ascomata with bright yellow or orange flat apices around the ostiole and hyaline ascospores (Fig. 2). These characteristics are consistent with the generic concept of *Byssosphaeria* (Barr 1990). Phylogenetic analyses of the combined LSU, SSU, ITS, and *tef-1α* sequence data showed that *B. chishuiense* (ACCC 35242) was sister to *B. villosa* (GKM 204N), and they reside within the Melanommataceae (Fig. 1). Although *B. chishuiense* and *B. villosa* have the same-sized asci (140–200 × 17–25 vs. 140–200 × 17–25 µm), *B. chishuiense* can be distinguished from *B. villosa* in having larger ascospores (41.5–51.5 × 7–9 vs. 30–40 × 8–12 µm) and ascomata (520–740 vs. 430–500 µm diam.) and the absence of appendages (Samuels and Müller 1978). The main morphological differences between

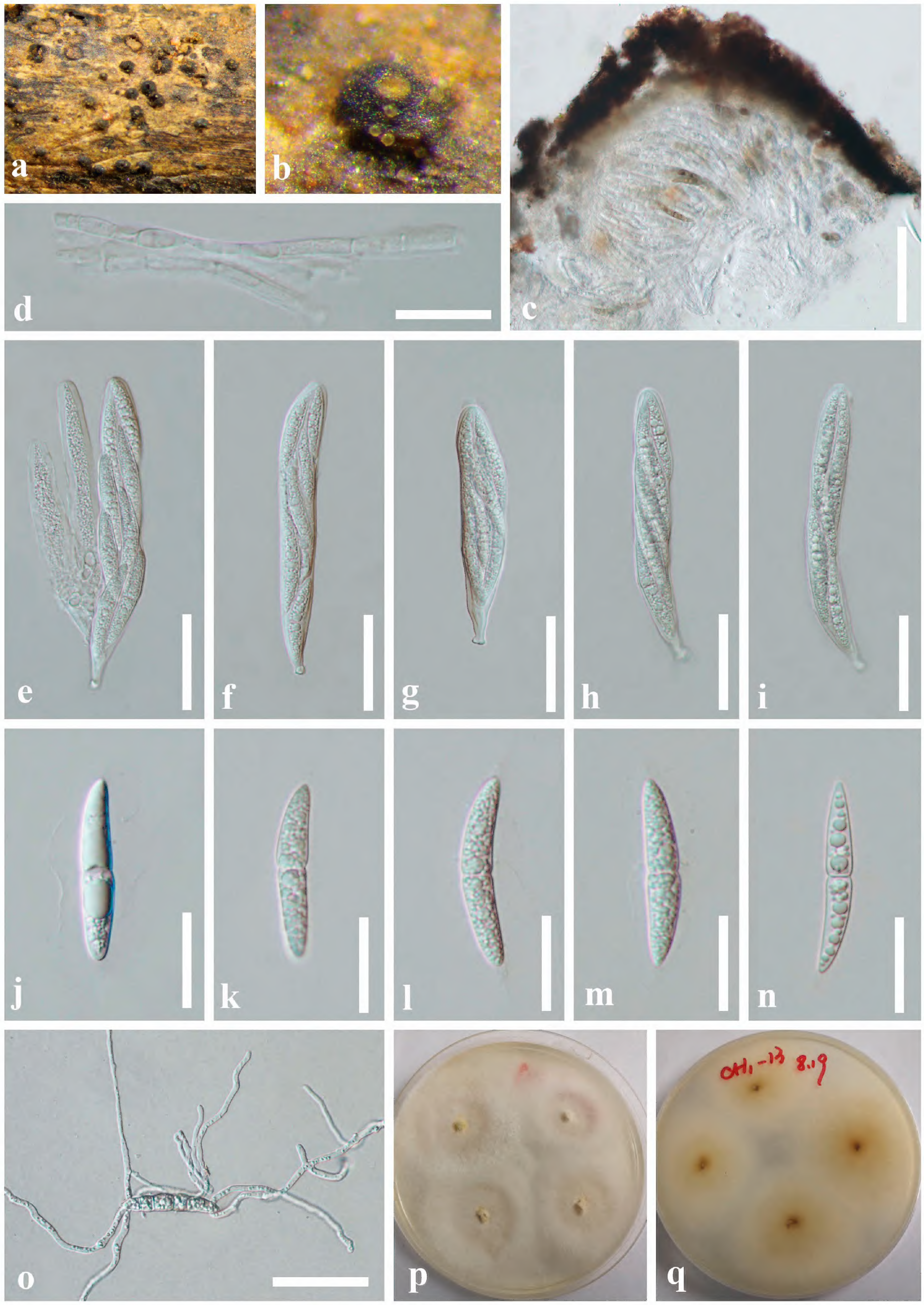

Figure 2. *Byssosphaeria chishuiense* (GZAAS 20-0374, holotype) **a, b** ascomata on natural substrate **c** section of an ascoma **d** pseudoparaphyses **e–i** asci **j–n** ascospores **o** germinated ascospore **p, q** culture from above and below, respectively. Scale bars: 50 µm (**b–o**).

Table 2. Synopsis of *Byssosphaeria* species.

Species	Ascomata Size high × diam. (μm)	Asci Size (μm)	Ascospores			References
			Size (μm)	Color	Septa	
Byssosphaeria alnea	220–460 diam.	105–140 × 7.5–12	19–24 × 4–5	Pale brown	1–3	Barr (1984)
B. chishuiense	**220–390 × 520–740**	**111–163 (–220) × 14–24.5**	**41.5–51.5 × 7–9**	**Hyaline**	**1–2**	**This study**
B. diffusa	340–480 × 300–450	80–110 × 9–12	16–20 × 4–6	Pale brown	1	Chen and Hsieh (2004)
B. erumpens	420–520 × 450–550	105–130 × 12–15	20–25 × 5–6	Dark brown	1	Chen and Hsieh (2004)
B. erythrinae	–	–	22–28 × 6–7.5	Hyaline to palebrown	1–3	Barr (1984)
B. hainanensis	182–291 × 165–280	115–130 × 7–11	10.5–14 × 3.5–5	Pale brown	1	Li and Zhuang (2008)
B. jamaicana	340–550 diam.	80–120 × 12–15	25–35 × 7–8	Light to clearbrown	1–3	Barr (1984)
B. juniper	220–400 diam.	100–145 × 12–18	18–27 × 6–9	Pale brown	3–4	Barr (1984)
B. keithii	350–520(–600) × (320–)400–620	80–112(–150)×10–13	80–112(–150) × 10–13	pale brown	1	Berkeley and Broome 1876; Tian et al. (2015)
B. macarangae	450–550 × 575–650	75–100 × 7–10	20–25 × 4–5	Hyaline	1(–3)	Tennakoon et al. (2018)
B. musae	430–540 × 450–630	125–135 × 12–14	30–33 × 5–6	Hyaline to light brown	1–3	Liu et al. (2015)
B. oviformis	1500–2000 × 1000–1500	120–130 × 7–9	25–30 × 2.5–3.5	Hyaline	1	Barr (1984)
B. phoenicis	580–625 × 600–650	100–160 × 10–15	25–30 × 5–7	Brick red to brown	3	Kularathnage et al. (2022)
B. rhodomphala	220–500 diam.	85–120 × 10–13	18–23 × 6–7.5	Light brown	1–(3)	Barr (1990)
B. salebrosa	440–800 diam.	120–150 × 13–16.5	40–50 × 7–9	Hyaline to light brown	1–3(–5)	Barr (1984)
B. schiedermayeriana	500–825; 423–511 × 478–537	100–150 × 12–15	32–42 × 5–8	Light brown	1–3(–5)	Barr (1984)
B. semen	400–600 × 330–550	80–110 × 9–12	20–30 × 3.5–4.5	Hyaline to pale brown	1–3	Barr (1984); Tian et al. (2015)
B. siamensis	501–692 × 561–720	112–148 × 10–16	40.5–50 × 7–11	Hyaline to pale yellow	1(–3)	Tian et al. (2015)
B. taiwanense	460–540 × 450–500	125–150 × 12–14	30–35 × 7–8	Pale to olivaceous brown	1	Tennakoon et al. (2018)
B. villosa	340–470 × 430–500	140–200 × 17–25	30–40 × 8–12	Hyaline to brown	1–2	Boise (1984); Samuels and Müller (1978)
B. xestothele	330–440 × 330–550	70–100 × 9–12	20–26 × 4.5–6	Hyaline to pale brown	1–3	Barr (1984)

Byssosphaeria spp. are detailed in Table 2. Additionally, comparing 828 nucleotides across the LSU gene region between *B. chishuiense* and *B. villosa* revealed 29 bp (3.50%) differences. Our molecular data also support that *B. chishuiense* and *B. villosa* are phylogenetically distinct (Fig. 1).

Byssosphaeria Cooke, Grevillea 7 (43): 84 (1879)

Synonym. *Neobyssosphaeria* Wanas., E.B.G. Jones & K.D. Hyde, Fungal Diversity 102: 57 (2020).

***Byssosphaeria clematidis* (Wanas., Phukhams., E.B.G. Jones & K.D. Hyde) L.L. Liu & Z.Y. Liu, comb. nov.**
Index Fungorum: IF557190
Facesoffungi Number: FoF07282

Basionym. *Neobyssosphaeria clematidis* Wanas, Phukhams., E. B. G. Jones, & K. D. Hyde, Fungal Diversity 102:57 (2020).

Material examined. UK • Hampshire, Botleywood, on dead stems of *Clematis vitalba*, 25 May, 2016, E.B.G. Jones, GJ 298 (MFLU 17-0614, holotype); • ex-type living culture, MFLUCC 17-0794.

Description. Phukhamsakda et al. (2020).

GenBank accession numbers. LSU: MT214566; SSU: MT408594.

Taxonomic notes. Phukhamsakda et al. (2020) introduced *Neobyssosphaeria*, which was grouped with *Byssosphaeria* to form a basal lineage in their phylogenetic analyses of combined LSU, SSU, and ITS sequence data. Morphologically, Phukhamsakda et al. (2020) distinguished *Neobyssosphaeria* from *Byssosphaeria* by immersed ascomata with central papilla filled with periphyses, cellular pseudoparaphyses, and broad fusiform and hyaline ascospores. However, these characters also exist in some *Byssosphaeria* species. For example, *B. siamensis* has ascomata with cellular pseudoparaphyses (Tian et al. 2015), and other species, such as *B. salebrosa* and *B. villosa*, have broad, fusiform, and hyaline ascospores (Samuels and Müller 1978; Barr 1984), being reminiscent of *Neobyssosphaeria clematidis* (Phukhamsakda et al. 2020). The only distinctive features are immersed ascomata in *Neobyssosphaeria* and superficial ascomata in *Byssosphaeria*. We regard it as not sufficient for the separation of these two genera (Sandoval-Denis et al. 2016; Sun et al. 2023). Additionally, in our phylogenetic analyses, *Neobyssosphaeria clematidis* formed an internal clade within *Byssosphaeria*. Therefore, we transfer *Neobyssosphaeria clematidis* to *Byssosphaeria* as *B. clematidis* and treat *Neobyssosphaeria* as a synonym of *Byssosphaeria*.

***Camposporium aquaticum* L.L. Liu & Z.Y. Liu, sp. nov.**
Index Fungorum: IF902546
Facesoffungi Number: FoF16381
Fig. 3

Etymology. Refers to the aquatic habitat of this fungus.

Holotype. GZAAS 20-0376.

Description. ***Saprobic*** on decaying, submerged wood in a freshwater habitat. ***Asexual morph*. *Colonies*** on natural substrate effuse, brown, procumbent. ***Mycelium*** partly immersed and partly superficial, composed of pale brown, septate, cylindrical hyphae. ***Conidiophores*** macronematous, mononematous, irregularly cylindrical, strongly flexuous to twisted, procumbent, brown, sometimes fading slightly towards the apex, smooth-walled, unbranched, thick-walled, 4–8–septate, 75–92 × 5.5–6.5 µm ($\bar{x}$ = 86 × 6 µm, n = 20). ***Conidiogenous cell***: holoblastic, monoblastic, integrated, terminal, cylindrical, pale brown. ***Conidia*** solitary, cylindrical to narrowly fusoid, elongate, subhyaline to pale olivaceous green when young, brown or pale brown

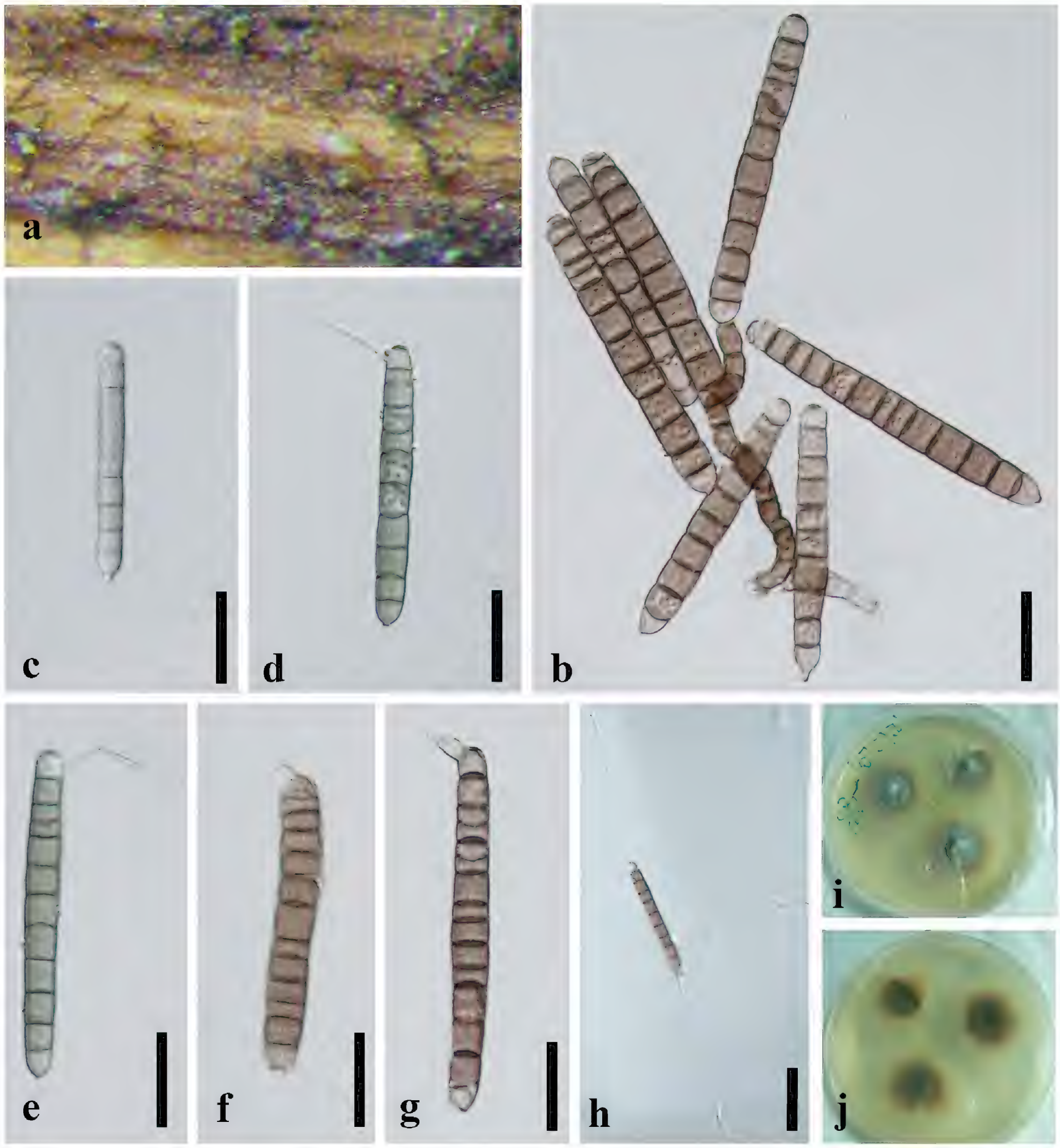

Figure 3. *Camposporium aquaticum* (GZAAS 20-0376, Herbarium) **a** colonies on natural substrate **b** conidiophore and conidium **c–g** conidia **h** germinating conidia **i, j** culture **i** from above **j** from below. Scale bars: 25 μm (**c–j**); 100 μm (**h**).

when mature, polar cells slightly paler, 64–114 × 7.5–11.5 μm ($\bar{x}$ = 91.5 × 9.5 μm, n = 30), smooth-walled, verruculose, 6–13-septate, often slightly constricted at the septa, basal cell conical, apical cell rounded with 2 independent, simple, cellular, aseptate, hyaline, smooth, straight, curved, or flexuous appendages, 29.5–40 × 1.5–2.5 μm ($\bar{x}$ = 33 × 1.8 μm, n = 20). ***Sexual morph*.** Undetermined.

Cultural characteristics. Conidia germinated on WA within 24 h, and germ tubes were produced from the apex. The colonies on PDA reached approximately

22 mm diam. after 3 weeks at 25 °C under dark conditions. Colonies circular, with raised center and filamentous edge, grey at center, brown at the edge from above, dark brown in the center, brown at the edge from reverse.

Material examined. CHINA • Guizhou Province, Guiyang City, Baihua Lake, near 26°39'18.20"N, 106°32'12.90"E, at 1205 m altitude, on a decaying branch submerged in the lake, 18 April, 2018, Lingling Liu, 18B-107 (GZAAS 20-0376, holotype); • ex-type living culture, ACCC 35528.

Taxonomic notes. Phylogenetic analyses of the combined LSU, SSU, ITS, and *tef1-α* sequence dataset showed that *C. aquaticum* (ACCC 35528) is sister to *C. guizhouense* (GZCC 19-0480) and formed a distinct lineage. We compared the base pair differences between the two new taxa and found six base pair differences (1.27%) across 471 nucleotides in the ITS gene region. Additionally, comparing the 972 nucleotides across the *tef1-α* gene region between ACCC 35528 and GZCC 19-0480 shows a 17 base pair difference (1.75%). Morphologically (Table 3), *C. aquaticum* (ACCC 35528) conidia resemble *C. guizhouense* conidia. However, *C. aquaticum* conidia (64–114 × 7.5–11.5 µm) are substantially larger than *C. guizhouense* conidia (58–81.5 × 7–9 µm), and *C. aquaticum* conidia are 6–13-septate, whereas *C. guizhouense* conidia are 8–11-septate (mostly 10). PHI analysis further confirmed that *C. aquaticum* (ACCC 35528) showed no significant genetic recombination with closely related species (Fw > 0.05, Fig. 4). Therefore, we introduce *C. aquaticum* (ACCC 35528) as a novel species.

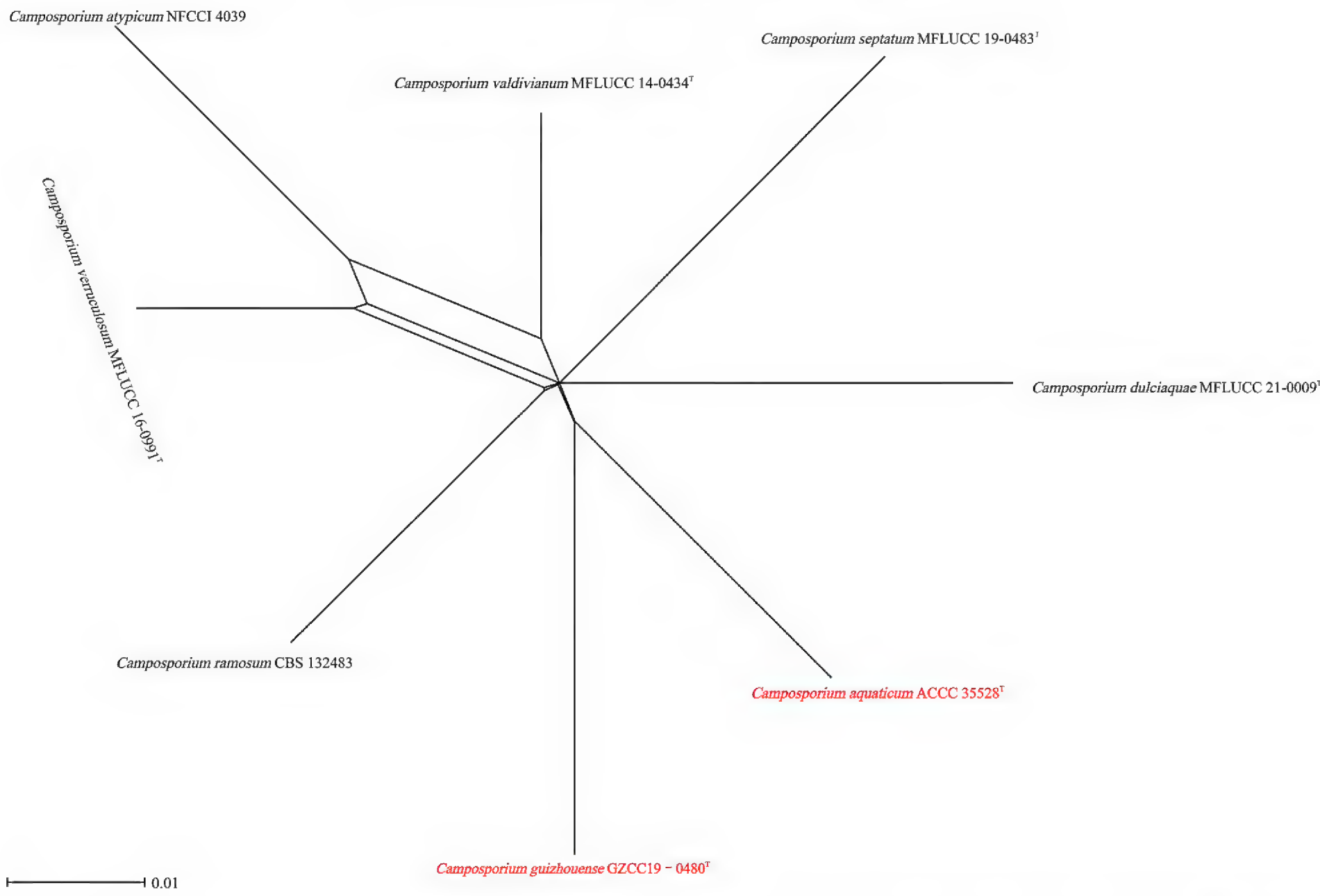
Campos porium atypicum NFCCI 4039
Campos porium septatum MFLUCC 19-0483T
Campos porium valdivianum MFLUCC 14-0434T
Campos porium verruculosum MFLUCC 16-0991T
Campos porium dulciaquae MFLUCC 21-0009T
Campos porium ramosum CBS 132483
Campos porium aquaticum ACCC 35528T
Campos porium guizhouense GZCC19 – 0480T
0.01

Figure 4. Split graphs showing the results of the PHI test of *C. aquaticum* (ACCC 35528^{T}) with their most closely related species (Fw = 0.9994). The new taxa are shown in red bold.

Table 3. Synopsis of *Camposporium* species.

Species name	Conidiophores		Conidia			Appendage			References
	Size (µm)	Septation	Size (µm)	Septation	Colour	Morphology	Septation	Length (µm)	
Camposporium antennatum	76–166 × 6	Up to 12	42–78 × 7.5–8.8	7–14 (4–14)	Pale–brown, paler end cells	1–3(simple)	Aseptate	Up to 40	Harkness (1884)
C. appendiculatum	very short	Septate	107–119 × 9.5–11.5	10–13	Pale–brown, hyaline at both end cells	1(simple)	Aseptate	72–114	Hyde et al. (2020)
C. aquaticum	**75–92 × 5.5–6.5 µm**	**4–8**	**64–114 × 7.5–11.5 µm**	**6–13**	**Brown, paler end cells**	**1 (simple)**	**Septate**		**This study**
C. atypicum	150–685 × 5–10	Septate	35–42 × 13–15	5–7	Brown, paler end cells	0	–	–	Koukol and Delgado (2021)
C. cambrense	22–84 × 6–7	3–10	62–115 × 8–10	Up to 15	Pale–brown, paler end cells	1(simple)	Septate	32–126	Hughes (1951)
C. dulciaquae	16–95 × 5–9	Septate	100–130 × 8.5–13	8–11	Brown, paler end cells	(2–)3 (simple)	Aseptate		Calabon et al. (2021)
C. fusisporum	100–145 × 6.5–10	10–15	86–115 × 13.5–19	8–11	Brown, paler end cells	2–3 (simple)	Aseptate	17–40	Whitton et al. (2002)
C. guizhouense	**60–110 × 4–6.5**	**3–9**	**58–81.5 × 7–9**	**8–11**	**Pale–brown, paler end cells**	**2 (simple)**	**Aseptate**	**24.5–47.5**	**This study**
C. hyalinum	10–40 × 4–6	0–1	20–75 × 3–5	2–6	Hyaline, concolourous	1 (simple)	Aseptate	16–55	Abdullah (1980)
C. hyderabadense	25.2–39.6 × 3.6–5.4	1–3	32.4–54 × 3.6–7.2	5–9	Dark–brown, concolourous	1–4 (simple)	Aseptate	Up to 43.2	Rama and Rao (1964)
C. indicum	28.5–50.4 × 3.6–7.2	2–5	21.6–72 × 3.6–7.2	3–14	Dark–brown, paler end cells	0	–	–	Rama and Rao (1964)
C. japonicum	37.5–77.5 × 5–6.5	5	42.5–70 × 5–7.5	7–10	Pale–brown, concolourous	0–1 (2–4–branched)	Aseptate	Up to 36	Ichinoe (1971)
C. laundonii	Up to 40 × 5–8	0–2	50–150 × 13–17	4–9	Brown, paler end cells	1–2 (simple)	Septate	Up to 60	Ellis (1976)
C. lycopodiellae	20–50 × 3–5	1–2	(65–)75–85(–100) × (7–)8(–9)	(7–)8–9(–11)	Pale–brown, hyaline at both end cells	0	–	–	Crous et al. (2018); Hyde et al. (2020a)
C. marylandicum	41–127 × 2–3	0–5	24.7–44 × 4.5–6.5	5–10	Hyaline, concolourous	1 (simple)	?	33.5–80	Shearer (1974)
C. microsporum	Up to 72 × 3.6–7.2	1–5	25.8–36 × 7.2–9	2–6	Pale–brown to brown, concolourous	1–2 (simple)	Aseptate	10.8–28.8	Rama and Rao (1964)
C. multiseptata	short	Septate	97–111 × 9–11	10–13	Dark–brown, paler end cells	1 (simple)	Septate	11–17	Hyde et al. (2020a)
C. ontariense	45–200 × 5–7	6–8	20–35 (20–53) × 8–12 (6.5–12)	3–7 (3–9)	Pale–brown, concolourous	0	–	–	Matsushima (1983)
C. pellucidum	30 to 150 × 5–8	Up to 10	78–140 × 7.5–12	Up to 16	Pale–brown, paler end cells	1(simple)	Septate	30–145	Hughes 1951; Hyde et al. (2020a)
C. quercicola	15–60 × 3.5–4	1–3	28–45 × 3.5–4.5	5–9	Pale–brown, paler end cells	0–3 (simple)	Aseptate	Up to 30	Mercado et al. (1995)
C. ramosum	70–138 × 5.2–6	4–10	80–112 × 6.4–9.6	8–15	Brown, paler end cells	1(1–3–branched)	1–2 septate	20–60	Whitton et al. (2002)
C. septatum	–	Septate	98–125 × 7–11.5	(8–)9 (–11)	Median brown, paler end cells	(2–)3 (simple)	Aseptate	–	Hyde et al. (2020a)
C. scolecosporium	10–20 × 2.5–4.5	0–3	48–108 × 3–4	6–12	Hyaline, concolourous	0	–	–	Kobayasi (1971)
C. valdivianum	91–114 × 8.5–11	7–9	38–40 × 12–15	7	Pale brown to dark brown, paler end cells	0	–	–	Li et al. (2017); Koukol and Delgado (2021)
C. verruculosum	49–65 × 5.5–7.5	1–3	59–66 × 15–18	8–10	Drown to dark brown, paler end cells	0	–	–	Li et al. (2017); Koukol and Delgado (2021)

***Camposporium guizhouense* L.L. Liu & Z.Y. Liu, sp. nov.**
Index Fungorum: IF902547
Facesoffungi Number: FoF15498
Fig. 5

Etymology. Refers to the location where the holotype was collected.

Holotype. GZAAS 20-0375.

Description. ***Saprobic*** on decaying, submerged wood in freshwater habitats. ***Asexual morph*. *Colonies*** on natural substrates are velvety, effuse, hairy, scattered, brown, and glistening. ***Mycelium*** partly immersed, partly superficial, hyaline to pale brown, septate, and cylindrical. ***Conidiophores*** macronematous, mononematous, irregularly cylindrical, straight to flexuous or twisted, erect, pale to mid-brown, sometimes fading slightly towards the apex, smooth-walled, unbranched, 3–9-septate, 60–110 × 4–6.5 µm ($\bar{x}$ = 80 × 5 µm, n = 20). ***Conidiogenous cells*** were holoblastic or polyblastic, integrated into the apical region of the conidiophore, denticulate, cylindrical, pale brown, smooth-walled, and sometimes attached to the conidia following detachment. ***Conidia*** solitary, cylindrical to narrowly fusoid, elongate, brown or pale brown, 58–81.5 × 7–9 µm ($\bar{x}$ = 70 × 8 µm, n = 20), paler at both ends, verrucose, thickened walls, 8–11-septate (mostly 10), basal cell conical with a truncate end, apical cell rounded with two independent, simple, cellular, aseptate, hyaline, smooth, straight, curved, or flexuous appendages, 24.5–47.5 × 1.5–3.5 µm ($\bar{x}$ = 35 × 2 µm, n = 20). ***Sexual morph*.** Undetermined.

Cultural characteristics. Conidia germinated on WA within 24 h, and germ tubes were produced from the apex. Colonies on PDA reached approximately 25 mm diam. after 3 weeks at 25 °C in dark, circular, grey-white, or yellowish mycelium, dense in the middle and sparse in the edge, in reverse, pale brown to brown, smooth in the margin.

Material examined. China • Guizhou Province, Guiyang City, Aha Lake, near 26°32'N, 106°40'E, at 1085 m altitude, on a decaying branch submerged in the lake, 16 April, 2018, L.L. Liu, 18A-8 (GZAAS 20-0375, holotype); • ex-type living culture, GZCC 19-0480.

Taxonomic notes. Phylogenetic analyses of the combined LSU, SSU, ITS, and *tef1-α* sequence dataset showed that *C. guizhouense* was sister to *C. ramosum* (CBS 132483) and formed a distinct lineage. We compared the *ITS* sequences of the new taxon (GZCC 19-0480) to that of *C. ramosum* (CBS 132483). A difference of 7.87% (37/470 bp) was observed. Additionally, comparing 812 nucleotides across the LSU gene region between GZCC 19-0480 and *C. ramosum* (CBS 132483) revealed 13 base pair differences (1.60%). Morphologically (Table 3), *C. guizhouense* conidia resemble *C. dulciaquae*, *C. fusisporum*, *C. ramosum*, and *C. septatum* conidia in shape. However, the conidia of *C. guizhouense* (58–81.5 × 7–9 µm) are considerably smaller than those of *C. dulciaquae*, *C. fusisporum*, *C. ramosum*, and *C. septatum* (100–130 × 8.5–13, 98–125 × 7–11.5, 80–112 × 6.4–9.6, and 86–115 × 13.5–19 µm, respectively). Moreover, the conidia of *C. guizhouense* have two simple and aseptate apical appendages; those of *C. dulciaquae*, *C. fusisporum*, and *C. septatum* have 2–3 apical appendages, and those of *C. ramosum* have 1–3 simple or branched septate appendages. Therefore, we introduce our collection as a new species, *C. guizhouense*.

Figure 5. *Camposporium guizhouense* (GZAAS 20-0375, Herbarium) **a, b** colonies on natural substrate **c, d** conidiophore and conidium **e, f** conidiophores **g–j** conidia **k** germinated conidium **l, m** culture **l** from above **m** from below. Scale bars: 50 µm (**c–j**).

Discussion

Over the last 20 years, freshwater ascomycetes have been extensively researched (Ranghoo and Hyde 1998; Ranghoo et al. 2000; Zhang et al. 2013; Luo et al. 2019; Calabon et al. 2020; Dong et al. 2020; Yang et al. 2023). Interestingly, molecular data were only used to resolve species in the early 2000s (Tsui et al. 2001; Jeewon et al. 2003; Kodsueb et al. 2004; Shearer et al. 2009, 2014; Hu et al. 2012; Hyde et al.2013; Boonmee et al. 2014; Cai et al. 2014; Yang et al. 2018). With the recent increasing availability and accessibility of molecular data, the number of identified species has increased rapidly, particularly in China and Thailand (Luo et al. 2018; Dong et al. 2020; Yang et al. 2023). Zhang et al. (2011) listed 173 species belonging to 112 genera recorded from freshwater habitats. Hu et al. (2013) reported 782 freshwater fungal species in China. Luo et al. (2019) identified 451 species belonging to 160 genera of freshwater Sordariomycetes. Dong et al. (2020) provided 145 genera of freshwater Dothideomycetes (six orders, 43 families), of which 32% (46 genera) were unique to freshwater habitats (Calabon et al. 2020; Dong et al. 2020), and Liu (2020) introduced 102 freshwater fungal species from 68 genera in karst wetlands in Guizhou Province, China. Recently, Yang et al. (2023) reported 47 new taxa, 7 new combinations, 10 new geographical records, and 9 habitat records collected from karst regions in China and Thailand. To the best of our knowledge, 68 new taxa of freshwater fungi have been reported in the karst regions of Guizhou Province, China (Liu et al. 2020; Yang et al. 2023). In this study, three novel taxa of freshwater ascomycetes from karst wetlands in Guizhou Province, China, were introduced based on combined multilocus phylogeny and morphological approaches. It appears that numerous new taxa await being discovered and described, as new freshwater habitats are explored, or a particular genus is being studied with molecular data, wherein its diversity is much higher than previously anticipated in China (Luo et al. 2019; Bao et al. 2020; Dong et al. 2020; Hyde et al. 2020b; Yang et al. 2023).

In this study, multi-gene phylogenetic analyses of Melanommataceae, including 28 genera with available sequence data for molecular comparisons, showed that *Byssosphaeria* and *Camposporium* are closely related and nested within Melanommataceae. *Byssosphaeria schiedermayeriana* is the first freshwater species in *Byssosphaeria* reported from Seychelles (Barr 1984), and this species has also been reported to exist in terrestrial habitats (Tian et al. 2015). Our species is the second freshwater species in *Byssosphaeria*. Contrarily, *Camposporium* species are more frequently found in freshwater habitats. The new taxon, *C. guizhouense* is the fifth freshwater species in this genus, and other 14 species recorded in freshwater habitats are *C. antennatum* (Rajashekhar and Kaveriappa 1996; Tsui et al. 2001; Smits et al. 2007), *C. appendiculatum* (Hyde et al. 2020a), *C. cambrense* (Gonczol and Revay 2004; Kurniawati et al. 2010; Gonczol and Revay 2011), *C. dulciaquae* (Calabon et al. 2021), *C. fusisporum* (Cai et al. 2003), *C. hyalinum* (Abdullah 1980), *C. japonicum* (Gonczol and Revay 2004; Gonczol and Revay 2011), *C. marylandicum* (Shearer 1974; Ingold 1976; Gonczol and Revay 1998), *C. multiseptatum* (Hyde et al. 2020a), *C. ontariense* (Gonczol and Revay 2004), *C. pellucidum* (Ingold 1976; Gonczol and Revay 1998; Gonczol and Revay 2004; Czeczuga et al. 2005; Smits et al. 2007; Gonczol and Revay 2011; Hyde et al. 2020a), *C. quercicola* (Cai et al. 2003), *C. septatum* (Hyde et al. 2020a), and *C. verruculosum* (Li et al. 2017; Koukol and Delgado 2021).

Phylogenetic analyses of Melanommataceae showed that *B. chishuiense* and *B. villosa* formed an independent and distinct lineage sister to other basal *Byssosphaeria* species. *Byssosphaeria villosa* was transferred from *Herpotrichia* (Samuels and Müller 1978), and its placement was confirmed subsequently (Mugambi and Huhndorf 2009; Tennakoon et al. 2018). The phylogenetic placement of *Byssosphaeria* in this study is similar to previous publications (Liu et al. 2015; Tian et al. 2015; Tennakoon et al. 2018), but its monophyly is not well supported, especially when *B. chishuiense* and *B. villosa* are involved. We temporarily accept these two species in *Byssosphaeria*, but more fresh collections are needed to resolve the taxonomic confusions of *Byssosphaeria*.

However, multi-gene phylogenetic analyses of Melanommataceae, which included all *Camposporium* strains, showed that *Camposporium* and *Fusiconidium* were grouped together within Melanommataceae. The placement of these two genera is consistent with the results of previous studies (Calabon et al. 2020; Hyde et al. 2020a). However, Calabon et al. (2020) and Hyde et al. (2020a) treated them as distinct genera based on morphological differences in conidiogenic cells and conidial shapes. Subsequently, Koukol and Delgado (2021) advocated that *Fusiconidium* is synonymous with *Camposporium* and listed numerous morphological similarities between them. For instance, *C. fusisporum* has fusiform conidia (Whitton et al. 2002), while the conidia of *C. ontariense* and *C. indicum* lack appendages. Moreover, *F. indicum* (Pratibha et al. 2017) has polyblastic conidiogenous cells with sympodial proliferation and slender, denticle-like separating cells, suggesting that these characteristics are similar to those of some species of *Camposporium* (Pratibha et al. 2017; Koukol and Delgado 2021). In this study, we accept that *Fusiconidium* combined *Camposporium*, *Fusiconidium aquaticum*, and *F. indicum* were renamed *C. verruculosum* and *C. atypicum*; *Fusiconidium lycopodiellae* and *F. mackenziei* were combined with *C. lycopodiellae* and *C. valdivianum* (Hyde et al. 2020a; Koukol and Delgado 2021).

Acknowledgments

Ling-Ling Liu thanks Ning-Guo Liu at the Guizhou Institute of Technology for his valuable modifications. Ling-Ling Liu thanks Jian-Kui Liu at the University of Electronic Science and Technology of China for valuable corrections and suggestions.

Additional information

Conflict of interest

The authors have declared that no competing interests exist.

Ethical statement

No ethical statement was reported.

Funding

This research was funded by the National Natural Science Foundation of China (project IDs: 32260007) and the 2023 Youth Foundation of Guizhou Academy of Agricultural Sciences (PhD Foundation) (project IDs: [2023] 09) and the "open list" project of Guizhou Academy of Agricultural Sciences (project IDs: Guizhou agricultural Science JBGS [2024-05].

Author contributions

Conceptualization, writing—original draft, data curation, and methodology: Ling-Ling Liu and Zuo-Yi Liu; Funding acquisition: Yong-Xiang Liu; Formal analysis: Ya-Ya Chen; Funding acquisition and project administration: Jiu-Lan Gou; Investigation and sample collection: Feng Chi, Yi Liu, and Meng Zhang; Software: Xiaofeng Gu and Quanquan Wei; Writing—review and editing: Si Zhou. All the authors have read and agreed to the published version of the manuscript.

Author ORCIDs

Ling-Ling Liu https://orcid.org/0000-0003-0006-0938
Ya-Ya Chen https://orcid.org/0000-0002-8293-168X
Jiu-Lan Gou https://orcid.org/0000-0001-6439-158X
Xiao-Feng Gu https://orcid.org/0000-0002-1197-2070
Quan-Quan Wei https://orcid.org/0000-0002-1672-1588
Meng Zhang https://orcid.org/0000-0002-3312-1402
Zuo-Yi Liu https://orcid.org/0000-0001-5348-8458

Data availability

The datasets generated for this study are available in the NCBI database.

References

Abdullah SK (1980) Two hyphomycetes on litter in stagnant water from Britain. Transactions of the British Mycological Society 75(3): 514–517. https://doi.org/10.1016/S0007-1536(80)80140-9

Bánki O, Roskov Y, Döring M, Ower G, Vandepitte L, Hobern D, Remsen D, Schalk P, De Walt RE, Keping M (2023) Catalogue of Life Checklist (Version 2023–01–12). Catalogue of Life. https://doi.org/10.48580/dfqz

Bao DF, McKenzie EHC, Bhat DJ, Hyde KD, Luo ZL, Shen HW, Su HY (2020) Acrogenospora (Acrogenosporaceae, Minutisphaerales) appears to be a very diverse genus. Frontiers in Microbiology 1606: 1606. https://doi.org/10.3389/fmicb.2020.01606

Barr ME (1984) Herpotrichia and its segregates. Mycotaxon 20: 1–38.

Barr ME (1990) Melanommatales (Loculoascomycetes). North American Flora Series (II): 1–129.

Beenken L, Gross A, Queloz V (2020) Phylogenetic revision of Petrakia and Seifertia (Melanommataceae, Pleosporales):New and rediscovered species from Europe and North America. Mycological Progress 19(5): 417–440. https://doi.org/10.1007/s11557-020-01567-7

Berkeley MJ, Broome CE (1876) Notices of British fungi. Annals & Magazine of Natural History 18(3): 128.

Boise JR (1984) New and interesting fungi (Loculoascomycetes) from the Amazon. Acta Amazonica 14: 49–53. https://doi.org/10.1590/1809-43921984145053

Boonmee S, Rossman AY, Liu JK, Li WJ, Dai DQ, Bhat JD, Jones EBG, McKenzie EHC, Xu JC, Hyde KD (2014) Tubeufiales, ord. nov., integrating sexual and asexual generic names. Fungal Diversity 68(1): 239–298. https://doi.org/10.1007/s13225-014-0304-7

Cai L, Zhang K, McKenzie EHC, Hyde KD (2003) Freshwater fungi from bamboo and wood submerged in the Liput River in the Philippines. FEMS Yeast Research 13(4): 1–12. https://doi.org/10.1016/S1567-1356(03)00107-7

Cai L, Hu DM, Liu F, Hyde KD, Jones EBG (2014) The molecular phylogeny of freshwater Sordariomycetes and Discomycetes. In: Jones EBG, Hyde KD, Pang KL (Eds) Freshwater Fungi and Fungal–like Organisms. De Gruyter, Berlin, 47–72. https://doi.org/10.1515/9783110333480.47

Calabon M, Hyde K, Jones E, Chandrasiri S, Dong W, Fryar S, Yang J, Luo ZL, Lu YZ, Bao DF, Boonmee S (2020) an online platform for the taxonomic classification of freshwater fungi. Asian Journal of Mycology 3(1): 419–445. https://doi.org/10.5943/ajom/3/1/14

Calabon MS, Jones EBG, Boonmee S, Doilom M, Lumyong SHKD, Hyde KD (2021) Five novel freshwater Ascomycetes indicate high undiscovered diversity in lotic habitats in Thailand. Journal of Fungi 7(2): 117. https://doi.org/10.3390/jof7020117

Capella-Gutiérrez S, Silla-Martínez JM, Gabaldón T (2009) trimAl: A tool for automated alignment trimming in large-scale phylogenetic analyses. Bioinformatics 25(15): 1972–1973. https://doi.org/10.1093/bioinformatics/btp348

Castañeda RRF (1985) Deuteromycotina de Cuba. Hyphomycetes III. Instituto de Investigaciones Fundamentales en Agricultura Tropical Alejandro de Humboldt, Habana, 42 pp.

Chen CY, Hsieh WH (2004) *Byssosphaeria* and *Herpotrichia* from Taiwan, with notes on the taxonomic relationship between these two genera. Sydowia 56: 24–38.

Cooke MC, Plowright CB (1879) British Sphaeriacei. Grevillea 7: 77–89. https://doi.org/10.1093/nq/s5-XII.292.89b

Crous PW, Schumacher PK, Wingfield MJ, Akulov A, Denman S, Roux J, Braun U, Burgess TI, Carnegie AJ, Váczy KZ, Guatimosim E, Schwartsburd PB, Barreto RW, Hernández-Restrepo M, Lombard L, Groenewald JZ (2018) New and interesting fungi. 1. Fungal Systematics and Evolution 1: 169–215. https://doi.org/10.3114/fuse.2018.01.08

Czeczuga B, Mazalska B, Godlewska A, Muszyńska E (2005) Aquatic fungi growing on dead fragments of submerged plants. Limnologica 35(4): 283–297. https://doi.org/10.1016/j.limno.2005.07.002

Dong W, Wang B, Hyde KD, McKenzie EHC, Raja HA, Tanaka K, Abdel-Wahab MA, Abdel-Aziz FA, Doilom M, Phookamsak R, Hongsanan S, Wanasinghe DN, Yu XD, Wang GN, Yang H, Yang J, Thambugala KM, Tian Q, Luo ZL, Yang JB, Miller AN, Fournier J, Boonmee S, Hu DM, Nalumpang S, Zhang H (2020) Freshwater Dothideomycetes. Fungal Diversity 105(1): 319–575. https://doi.org/10.1007/s13225-020-00463-5

Dudka IA (1966) New and rare species of fungi imperfecti from the basins of the southern part of Kiev Polessye. Ukrainian Botanical Journal 23: 91–95.

Ellis MB (1971) Dematiaceous Hyphomycetes. Commonwealth Mycological Institute, Kew, UK. https://doi.org/10.1079/9780851986180.0000

Ellis MB (1976) More Dematiaceous Hyphomycetes. Commonwealth Mycological Institute, Kew, 1–507. https://doi.org/10.1079/9780851983653.0000

Gao Y, Zhong TF, Bhat JD, Gomes de Farias AR, Dawoud TM, Hyde KD, Xiong WQ, Li YJ, Gui H, Yang XF, Wu SX, Wanasinghe DN (2023) Pleomorphic *Dematiomelanomma yunnanense* gen. et sp. nov. (Ascomycota, Melanommataceae) from grassland vegetation in Yunnan, China. MycoKeys 98: 273–297. https://doi.org/10.3897/mycokeys.98.107093

Glez-Peña D, Gómez-Blanco D, Reboiro-Jato M, Fdez-Riverola F, Posada D (2010) FALTER: Program oriented conversion of DNA and protein alignments. Nucleic Acids Research 38: 14–18. https://doi.org/10.1093/nar/gkq321

Gonczol J, Revay A (1998) Aquatic hyphomycetes in a tributary of the Morgo stream, Borzsony Mts, NE Hungary. Studia Botanica Hungarica 29: 5–16.

Gonczol J, Revay A (2004) Fungal spores in rainwater: Stemflow, throughfall and gutter conidial assemblages. Fungal Diversity 16: 67–86. https://doi.org/10.1023/B:MYCO.0000041833.41085.6f

Gonczol J, Revay A (2011) Aquatic hyphomycetes and other water–borne fungi in Hungary. Czech Mycology 63(2): 133–151. https://doi.org/10.33585/cmy.63203

Hall TA (1999) BioEdit: A user–friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. Nucleic Acids Symposium Series 41: 95–98. https://doi.org/10.1021/bk-1999-0734.ch008

Harkness HW (1884) New species of Californian fungi. Bulletin of the California Academy of Sciences 1: 29–47.

Hashimoto A, Matsumura M, Hirayama K, Fujimoto R, Tanaka K (2017) Pseudodidymellaceae fam. nov.:Phylogenetic affiliations of mycopappus–like genera in Dothideomycetes. Studies in Mycology 87(1): 187–206. https://doi.org/10.1016/j.simyco.2017.07.002

Hawksworth DL, Kirk PM, Sutton BC, Pegler DN (1995) Ainsworth & bisby's dictionary of the fungi, 8th edn. CABI, Wallingford.

Hongsanan S, Hyde KD, Phookamsak R, Wanasinghe DN, McKenzie EHC, Sarma VV, Lücking R, Boonmee S, Bhat JD, Liu N, Tennakoon DS, Pem D, Karunarathna A, Jiang S, Jones GEB, Phillips AJL, Manawasinghe IS, Tibpromma S, Jayasiri SC, Sandamali D, Jayawardena RS, Wijayawardene NN, Ekanayaka AH, Jeewon R, Lu Y, Phukhamsakda C, Dissanayake AJ, Zeng X, Luo Z, Tian Q, Thambugala KM, Dai D, Samarakoon MC, Chethana KWT, Ertz D, Doilom M, Liu J, Pérez-Ortega S, Suija A, Senwanna C, Wijesinghe SN, Niranjan M, Zhang S-N, Ariyawansa HA, Jiang H-B, Zhang J-F, Norphanphoun C, de Silva NI, Thiyagaraja V, Zhang H, Bezerra JDP, Miranda-González R, Aptroot A, Kashiwadani H, Harishchandra D, Sérusiaux E, Abeywickrama PD, Bao D-F, Devadatha B, Wu H-X, Moon KH, Gueidan C, Schumm F, Bundhun D, Mapook A, Monkai J, Bhunjun CS, Chomnunti P, Suetrong S, Chaiwan N, Dayarathne MC, Yang J, Rathnayaka AR, Xu J-C, Zheng J, Liu G, Feng Y, Xie N (2020) Refined families of Dothideomycetes: Orders and families incertae sedis in Dothideomycetes. Fungal Diversity 105(1): 17–318. https://doi.org/10.1007/s13225-020-00462-6

Hu DM, Chen H, Cai L, Bahkali AH, Hyde KD (2012) *Aquapeziza*: A new genus from freshwater and its morphological and phylogenetic relationships to Pezizaceae. Mycologia 104(2): 540–546. https://doi.org/10.3852/11-123

Hu DM, Liu F, Cai L (2013) Biodiversity of aquatic fungi in China. Mycology 4(3): 125–168. https://doi.org/10.1080/21501203.2013.835752

Hughes SJ (1951) Studies on micro–fungi. III. *Mastigosporium*, *Camposporium*, and *Ceratophorum*. Mycological Papers 36: 1–43.

Hyde KD, Jones EBG, Liu JK, Ariyawansa H, Boehm E, Boonmee S, Braun U, Chomnunti P, Crous PW, Dai DQ, Diederich P, Dissanayake A, Doilom M, Doveri F, Hongsanan S, Jayawardena R, Lawrey JD, Li YM, Liu YX, Lücking R, Monkai J, Muggia L, Nelsen MP, Pang KL, Phookamsak R, Senanayake IC, Shearer CA, Suetrong S, Tanaka K, Thambugala KM, Wijayawardene NN, Wikee S, Wu HX, Zhang Y, Aguirre-Hudson B, Alias SA, Aptroot A, Bahkali AH, Bezerra JL, Bhat DJ, Camporesi E, Chukeatirote E, Gueidan C, Hawksworth DL, Hirayama K, Hoog SD, Kang JC, Knudsen K, Li WJ, Li XH, Liu ZY, Mapook A, McKenzie EHC, Miller AN, Mortimer PE, Phillips AJL, Raja HA, Scheuer C, Schumm F, Taylor JE, Tian Q, Tibpromma S, Wanasinghe DN, Wang Y, Xu JC, Yacharoen S, Yan JY, Zhang M (2013) Families of Dothideomycetes. Fungal Diversity 63(1): 1–313. https://doi.org/10.1007/s13225-013-0263-4

Hyde KD, Jones EBG, Camporesi E, McKenzie EHC, Hongsanan S, Phookamsak R, Luo ZL, Boonmee S, Li WJ, Dissanayake AJ, Jayasiri SC, Su HY, Zhao Q, Lu YZ, Wanasinghe DN, Phukhamsakda C, Norphanphoun C, Lee HB, Kytövuori I, Lin CG, Mapook A, Tanaka K, Senanayake IC, Raj KNA, Perera RH, Doilom M, Tibpromma S, Huang SK, Thambugala

KM, Neta A, Zhang JF, Liu ZY, Ghosh A, Sandaruwan D, Yang J, Mafalda-Freire F, Daranagama DA, Papizadeh M, Tian Q, Wijayawardene NN, Chomnunti P, Ariyawansa HA, Ekanayaka AH, de Silva NI, Thongbai B, Cui BK, Uniyal P, de Azevedo Santiago ALCM, Zeng XY, Jayawardena RS, Konta S, Abdel-Wahab MA, Hashimoto A, Zhang H, Wu H, Shang QJ, Goh TK, Dayarathne MC, Lantieri A, Liu JK, Niskanen T, Liimatainen K, Kamolhan S, Banmai S, Bulgakov TS, Nguyen TTT, Bhat DJ, Drechsler-Santos R, Buyck B, Baghela A, Das K, Reck MA, Soudi MR, Manimohan P, Stadler M, Richter C, Kirk PM, Bahkali AH, Abdel-Aziz FA, Takahashi T, Wang Y, Karunarathna SC, Lücking R, Vizzini A, Medardi G, Shahzadeh Fazeli SA, Gibertoni TB, Wulandari NF, Duong TT, Li J, Manawasinghe IS, Bojantchev D, Ammirati JF, Bhatt RP, de Lima CLF, de Souza CAF, Wen TC, Tangthirasunun N, Dai YC, Zhou JL, Zhu L, de Oliveira RJV, Mortimer PE, Xu J, Ercole E (2016) Fungal diversity notes 367–490: Taxonomic and phylogenetic contributions to fungal taxa. Fungal Diversity 80: 1–270. https://doi.org/10.1007/s13225-016-0373-x

Hyde KD, Dong Y, Phookamsak R, Jeewon R, Bhat DJ, Jones EBG, Liu NG, Abeywickrama PD, Mapook A, Wei DP, Perera RH, Manawasinghe IS, Pem D, Bundhun D, Karunarathna A, Ekanayaka AH, Bao DF, Li JF, Samarakoon MC, Chaiwan N, Lin CG, Phutthacharoen K, Zhang SN, Senanayake IC, Goonasekara ID, Thambugala KM, Phukhamsakda C, Tennakoon DS, Jiang HB, Yang J, Zeng M, Huanraluek N, Liu JK, Wijesinghe SN, Tian Q, Tibpromma S, Brahmanage RS, Boonmee S, Huang SK, Thiyagaraja V, Lu YZ, Jayawardena RS, Dong W, Yang EF, Singh SK, Singh SM, Rana S, Lad SS, Anand G, Devadatha B, Niranjan M, Sarma VV, Liimatainen K, Aguirre-Hudson B, Niskanen T, Overall A, Alvarenga RLM, Gibertoni TB, Pfliegler WP, Horváth E, Imre A, Alves AL, Santos ACS, Tiago PV, Bulgakov TS, Wanasinghe DN, Bahkali AH, Doilom M, Elgorban AM, Maharachchikumbura SSN, Rajeshkumar KC, Haelewaters D, Mortimer PE, Zhao Q, Lumyong S, Xu JC, Sheng J (2020a) Fungal diversity notes 1151–1276. Fungal Diversity 100(1): 5–277. https://doi.org/10.1007/s13225-020-00439-5

Hyde KD, Jeewon R, Chen YJ, Bhunjun CS, Calabon MS, Jiang HB, Lin CG, Norphanphoun C, Sysouphanthong P, Pem D, Tibpromma S, Zhang Q, Doilom M, Jayawardena RS, Liu JK, Maharachchikumbura SSN, Phukhamsakda C, Phookamsak R, Al-Sadi AM, Thongklang N, Wang Y, Gafforov Y, Jones EBG, Lumyong S (2020b) The numbers of fungi: Is the descriptive curve flattening? Fungal Diversity 103(1): 219–271. https://doi.org/10.1007/s13225-020-00458-2

Ichinoe M (1971) Camposporium species from Japan. Nippon Kingakkai Kaiho 12: 79–88.

Index Fungorum (2024) Index Fungorum. http://www.indexfungorum.org/names/names.asp [accessed on 20 July 2024]

Ingold CT (1976) *Camposporium marylandicum* shearer from Britain. Transactions of the British Mycological Society 67(3): 532–533. https://doi.org/10.1016/S0007-1536(76)80191-X

Jayasiri SC, Hyde KD, Ariyawansa HA, Bhat DJ, Buyck B, Cai L, Dai Y, Abd–Elsalam KA, Ertz D, Hidayat I, Jeewon R, Jones EBG, Bahkali AH, Karunarathna SC, Liu JK, Luangsa-ard JJ, Lumbsch HT, Maharachchikumbura SSN, McKenzie EHC, Moncalvo JM, Ghobad-Nejhad M, Nilsson H, Pang KL, Pereira OL, Phillips AJL, Raspé O, Rollins AW, Romero AI, Etayo J, Selçuk F, Stephenson SL, Suetrong S, Taylor JE, Tsui CKM, Vizzini A, Abdel-Wahab MA, Wen TC, Boonmee S, Dai DQ, Daranagama DA, Dissanayake AJ, Ekanayaka AH, Fryar SC, Hongsanan S, Jayawardena RS, Li WJ, Perera RH, Phookamsak R, de Silva NI, Thambugala KM, Tian Q, Wijayawardene NN, Zhao RL, Zhao Q, Kang JC, Promputtha I (2015) The faces of fungi database: Fungal names linked with morphology, phylogeny and human impacts. Fungal Diversity 74(1): 3–18. https://doi.org/10.1007/s13225-015-0351-8

Jeewon R, Cai L, Liew ECY, Zhang KQ, Hyde KD (2003) *Dyrithiopsis lakefuxianensis* gen. et sp. nov. from Fuxian Lake, Yunnan, China, and notes on the taxonomic confusion surrounding Dyrithium. Mycologia 95(5): 911–920. https://doi.org/10.1080/15572536.2004.11833050

Katoh K, Standley DM (2013) MAFFT multiple sequence alignment software version 7: Improvements in performance and usability. Molecular Biology and Evolution 30(4): 772–780. https://doi.org/10.1093/molbev/mst010

Kirk PM, Cannon PF, David JC, Stalpers JA (2001) Dictionary of the fungi, 9th edn. CABI Publishing, Wallingford, 655.

Kobayasi Y (1971) Mycological reports from New Guinea and the Solomon Islands (1–11). Bulletin of the National Science Museum, Tokyo 14(3): 367–551.

Kodsueb R, Lumyong S, Lumyong P, McKenzie EHC, Ho WH, Hyde KD (2004) *Acanthostigma* and *Tubeufia* species, including *T. claspisphaeria* sp. nov. from submerged wood in Hong Kong. Mycologia 96(3): 667–674. https://doi.org/10.1080/15572536.2005.11832963

Koukol O, Delgado G (2021) Why morphology matters: The negative consequences of hasty descriptions of putative novelties in asexual ascomycetes. IMA Fungus 12(1): 26. https://doi.org/10.1186/s43008-021-00073-z

Kularathnage ND, Wanasinghe DN, Senanayake IC, Yang Y, Manawasinghe IS, Phillips AJL, Hyde KD, Dong W, Song J (2022) Microfungi associated with ornamental palms: *Byssosphaeria phoenicis* sp.nov. (Melanommataceae) and *Pseudocoleophoma rhapidis* sp. nov. (Dictyosporiaceae) from south China. Phytotaxa 568(2): 149–169. https://doi.org/10.11646/phytotaxa.568.2.2

Kurniawati E, Zhang H, Chukeatirote E, Sulistyowati L, Moslem MA, Hyde KD (2010) Diversity of freshwater ascomycetes in freshwater bodies at Amphoe Mae Chan, Chiang Rai. Cryptogamie. Mycologie 31: 323–331. https://doi.org/10.1016/j.riam.2010.05.002

Larget B, Simon DL (1999) Markov Chain Monte Carlo algorithms for the Bayesian analysis of phylogenetic trees. Molecular Biology and Evolution 16(6): 750–759. https://doi.org/10.1093/oxfordjournals.molbev.a026160

Li WY, Zhuang WY (2008) Notes on the genus *Byssosphaeria* (Melanommataceae) from China. Mycosystema 27: 48–53.

Li JF, Jeewon R, Luo ZL, Phookamsak R, Bhat DJ, Mapook A, Phukhamsakda C, Camporesi E, Lumyong S, Hyde KD (2017) Morphological characterization and DNA based taxonomy of *Fusiconidium* gen. nov. with two novel taxa within Melanommataceae (Pleosporales). Phytotaxa 308(2): 206–218. https://doi.org/10.11646/phytotaxa.308.2.2

Liew ECY, Aptroot A, Hyde KD (2000) Phylogenetic significance of the pseudoparaphyses in Loculoascomycete taxonomy. Molecular Phylogenetics and Evolution 16(3): 392–402. https://doi.org/10.1006/mpev.2000.0801

Liu LL (2020) Diversity and Phylogeny of Freshwater Fungi inWetland of Guizhou Karst Plateau [dissertation]. Guiyang (China): Guizhou University.

Liu JK, Hyde KD, Jones EBG, Ariyawansa HA, Bhat DJ, Boonmee S, Maharachchikumbura SSN, McKenzie EHC, Phookamsak R, Phukhamsakda C, Shenoy BD, Abdel-Wahab MA, Buyck B, Chen J, Chethana KWT, Singtripop C, Dai DQ, Dai YC, Daranagama DA, Dissanayake AJ, Doilom M, D'souza MJ, Fan XL, Goonasekara ID, Hirayama K, Hongsanan S, Jayasiri SC, Jayawardena RS, Karunarathna SC, Li WJ, Mapook A, Norphanphoun C, Pang KL, Perera RH, Peršoh D, Pinruan U, Senanayake IC, Somrithipol S, Suetrong S, Tanaka K, Thambugala KM, Tian Q, Tibpromma S, Udayanga D,

Wijayawardene NN, Wanasinghe D, Wisitrassameewong K, Zeng XY, Abdel-Aziz FA, Adamčík S, Bahkali AH, Boonyuen N, Bulgakov T, Callac P, Chomnunti P, Greiner K, Hashimoto A, Hofstetter V, Kang JC, Lewis D, Li XH, Liu XZ, Liu ZY, Matsumura M, Mortimer PE, Rambold G, Randrianjohany E, Sato G, Sri-Indrasutdhi V, Tian CM, Verbeken A, von Brackel W, Wang Y, Wen TC, Xu JC, Yan JY, Zhao RL, Camporesi E (2015) Fungal Diversity Notes 1–110: Taxonomic and phylogenetic contributions to fungal species. Fungal Diversity 72(1): 1–197. https://doi.org/10.1007/s13225-015-0324-y

Liu LL, Liu NG, Yang J, Chen YY, Gui XX, Liu ZY (2019) *Sporidesmium guizhouense* sp. nov. (Sordariomycetes incertae sedis), a new species from a freshwater habitat in Guizhou Province, China. Phytotaxa 422: 144–156. https://doi.org/10.11646/phytotaxa.422.2.2

Liu LL, Liu NG, Yang J, Chen YY, Liu ZY (2020) *Cucurbitinus* gen. nov. (Halosphaeriaceae, Microascales), a new genus to accommodate *Cucurbitinus constrictus* comb. nov. and *Cucurbitinus ibericus* comb. nov. Phytotaxa 455: 119–136. https://doi.org/10.11646/phytotaxa.455.2.4

Liu LL, Feng Y, Wei QQ, Zhang M, Gu, XF, Liu ZY, Gou JL (2023a) *riplosphaeria guizhouensis* sp. nov. (Tetraplosphaeriaceae, Pleosporales), a novel taxon from freshwater habitat in Guizhou Province, China. Phytotaxa 603(2): 173–183. https://doi.org/10.11646/phytotaxa.603.2.4

Liu LL, Song LC, Gu, XF, Wei QQ, Zhang M, Liu ZY, Gou JL (2023b) *Dictyosporium duliujiangense* sp. nov. (Dictyosporiaceae, Pleosporales) from freshwater habitat in Guizhou Province, China. Phytotaxa 606(4): 259–272. https://doi.org/10.11646/phytotaxa.606.4.2

Liu LL, Yang J, Zhou S, Gu, XF, Gou JL, Wei QQ, Zhang M, Liu ZY (2023c) Novelties in Microthyriaceae (Microthyriales): Two New Asexual Genera with Three New Species from Freshwater Habitats in Guizhou Province, China. Journal of Fungi 9: 178. https://doi.org/10.3390/jof9020178

Luo ZL, Hyde KD, Liu JK, Bhat DJ, Bao DF, Li WL, Su HY (2018) Lignicolous freshwater fungi from China II: Novel *Distoseptispora* (Distoseptisporaceae) species from northwestern Yunnan Province and a suggested unified method for studying lignicolous freshwater fungi. Mycosphere 9(3): 444–461. https://doi.org/10.5943/mycosphere/9/3/2

Luo ZL, Hyde KD, Liu JK, Maharachchikumbura SSN, Jeewon R, Bao DF, Bhat DJ, Lin CG, Li WL, Yang J, Liu NG, Lu YZ, Jayawardena RS, Li JF, Su HY (2019) Freshwater Sordariomycetes. Fungal Diversity 99(1): 451–660. https://doi.org/10.1007/s13225-019-00438-1

Matsushima T (1971) Some interesting fungi imperfecti. Bulletin of the National Science Museum, Tokyo 14: 460–480.

Matsushima T (1983) Matsushima mycological memoirs No. 3. Published by the author, Kobe, Japan. https://doi.org/10.2307/3793127

Mercado SA, Heredia G, Mena PJ (1995) ew species of dematiaceous hyphomycetes from Veracruz, Mexico. Mycotaxon 55: 491–499.

Miller MA, Pfeiffer W, Schwartz T (2010) Creating the CIPRES Science Gateway for inference of large phylogenetic trees. In: Proceedings of the 2010 Gateway Computing Environments Workshop (GCE); 2010 Nov. 14; New Orleans, LA, USA, 1–8. https://doi.org/10.1109/GCE.2010.5676129

Mugambi GK, Huhndorf SM (2009) Molecular phylogenetics of Pleosporales:Melanommataceae and Lophiostomataceae recircumscribed (Pleosporomycetidae, Dothideomycetes, Ascomycota). Studies in Mycology 64: 103–121. https://doi.org/10.3114/sim.2009.64.05

Nylander JA, Wilgenbusch JC, Warren DL, Swofford DL (2008) AWTY (are we there yet?): A system for graphical exploration of MCMC convergence in Bayesian phylogenetics. Bioinformatics 24(4): 581–583. https://doi.org/10.1093/bioinformatics/btm388

Phukhamsakda C, McKenzie EHC, Phillips AJL, Jones EBG, Bhat DJ, Stadler M, Bhunjun CS, Wanasinghe DN, Thongbai B, Camporesi E, Ertz D, Jayawardena RS, Perera RH, Ekanayake AH, Tibpromma S, Doilom M, Xu JC, Hyde KD (2020) Microfungi associated with Clematis (Ranunculaceae) with an integrated approach to delimiting species boundaries. Fungal Diversity 102(1): 1–203. https://doi.org/10.1007/s13225-020-00448-4

Pratibha J, Ashish P, Mao AA (2017) *Fusiconidium indicum* (Melanommataceae) a novel species of asexual Ascomycetes. Phytotaxa 326(2): 108–114. https://doi.org/10.11646/phytotaxa.326.2.2

Rajashekhar M, Kaveriappa KM (1996) Studies on the aquatic hyphomycetes of a sulfur spring in the Western Ghats, India. Microbial Ecology 32(1): 73–80. https://doi.org/10.1007/BF00170108

Rambaut A (2012) FigTree v1. 4.0. A Graphical Viewer of Phylogenetic Trees. http://tree.bio.ed.ac.uk/software/figtree/ [accessed on 1 August 2024]

Ranghoo VM, Hyde KD (1998) Ascomycetes from freshwater habitats:*Ascolacicola aquatica* gen. et sp. nov. and a new species of *Ascotaiwania* from wood submerged in a reservoir in Hong Kong. Mycologia 90(6): 1055–1062. https://doi.org/10.1080/00275514.1998.12027005

Ranghoo VM, Hyde KD, Wong SW, Tsui CKM, Jones EBG (2000) *Vertexicola caudatus* gen. et sp. nov., and a new species of *Rivulicola* from submerged wood in freshwater habitats. Mycologia 92(5): 1019–1026. https://doi.org/10.1080/00275514.2000.12061245

Rao PR, Rao D (1964) Some species of *Camposporium* Harkn. from India. Antonie van Leeuwenhoek 30(1): 60–64. https://doi.org/10.1007/BF02046701

Rehner SA, Buckley EA (2005) *Beauveria* phylogeny inferred from nuclear ITS and EF1–alpha sequences: Evidence for cryptic diversification and links to *Cordyceps* teleomorphs. Mycologia 97(1): 84–98. https://doi.org/10.1080/15572536.2006.11832842 [TEF.]

Rehner SA, Samuels GJ (1994) Taxonomy and phylogeny of *Gliocladium* analysed from nuclear large subunit ribosomal DNA sequences. Mycological Research 98(6): 625–634. https://doi.org/10.1016/S0953-7562(09)80409-7

Ronquist F, Teslenko M, Van Der Mark P, Ayres DL, Darling A, Höhna S, Larget B, Liu L, Suchard MA, Huelsenbeck JP (2012) MrBayes 3.2:Efficient Bayesian phylogenetic inference and model choice across a large model space. Systematic Biology 61(3): 539–542. https://doi.org/10.1093/sysbio/sys029

Samuels GJ, Müller E (1978) Life–history studies of Brazilian ascomycetes 4. Three species of Herpotricia and their Pyrenochaeta– like anamorphs. Sydowia 31: 157–168.

Sandoval-Denis M, Gené J, Sutton DA, Cano-Lira JF, de Hoog GS, Decock CA, Wiederhold NP, Guarro J (2016) Redefining Microascus, Scopulariopsis and allied genera. Persoonia 36(1): 1–36. https://doi.org/10.3767/003158516X688027

Senanayake IC, Rathnayaka AR, Marasinghe DS, Calabon MS, Gentekaki E, Lee HB, Hurdeal VG, Pem D, Dissanayake LS, Wijesinghe SN, Bundhun D, Nguyen TT, Goonasekara ID, Abeywickrama PD, Bhunjun CS, Jayawardena RS, Wanasinghe DN, Jeewon R, Bhat DJ, Xiang MM (2020) Morphological approaches in studying fungi: Collection, examination, isolation, sporulation and preservation. Mycosphere 11(1): 2678–2754. https://doi.org/10.5943/mycosphere/11/1/20

Shearer CA (1974) Fungi of the Chesapeake Bay and its tributaries IV. Three new species from the Patuxent River. Mycologia 66(1): 16–24. https://doi.org/10.1080/00275514.1974.12019568

Shearer CA, Raja HA, Miller AN, Nelson P, Tanaka K, Hirayama K, Marvanová L, Hyde KD, Zhang Y (2009) The molecular phylogeny of freshwater Dothideomycetes. Studies in Mycology 64: 145–153. https://doi.org/10.3114/sim.2009.64.08

Shearer CA, Pang KL, Suetrong S, Raja RA (2014) Phylogeny of the Dothideomycetes and other classes of freshwater fissitunicate Ascomycota. In: Jones EBG, Hyde KD, Pang KL (Eds) Freshwater Fungi and Fungal–like Organisms. De Gruyter, Berlin, 25–45. https://doi.org/10.1515/9783110333480.25

Sivanesan A (1984) The bitunicate ascomycetes and their anamorphs. Athens. International Journal of Middle East Studies 41: 510–512. https://doi.org/10.1017/S002074380909134X

Smits G, Fernández R, Cressa C (2007) Preliminary study of aquatic hyphomycetes from Venezuelan streams. Acta Botanica Venezuelica 30: 345–355.

Stamatakis A (2014) RAxML Version 8: A tool for phylogenetic analysis and post–analysis of large phylogenies. Bioinformatics 30(9): 1312–1313. https://doi.org/10.1093/bioinformatics/btu033

Sun YR, Zhang JY, Hyde KD, Wang Y, Jayawardena RS (2023) Morphology and Phylogeny Reveal Three Montagnula Species from China and Thailand. Plants 12(4): 738. https://doi.org/10.3390/plants12040738

Tennakoon DS, Jeewon R, Chang-Hsin K, Hyde KD (2018) Phylogenetic and morphological characterization of *Byssosphaeria macarangae* sp. nov., and *B. taiwanense* sp. nov. from Macaranga tanarius. Phytotaxa 364(3): 211–226. https://doi.org/10.11646/phytotaxa.364.3.1

Tian Q, Liu JK, Hyde KD, Wanasinghe DN, Boonmee S, Jayasiri SC, Luo ZL, Taylor JE, Phillips AJL, Bhat DJ, Li WJ, Ariyawansa H, Thambugala KM, Jones EBG, Chomnunti P, Bahkali AH, Xu JC, Camporesi E (2015) Phylogenetic relationships and morphological reappraisal of Melanommataceae (Pleosporales). Fungal Diversity 74(1): 267–324. https://doi.org/10.1007/s13225-015-0350-9

Tibpromma S, Hyde KD, Jeewon R, Maharachchikumbura SSN, Liu JK, Bhat DJ, Jones EBG, McKenzie EHC, Camporesi E, Bulgakov TS, Doilom M, de Azevedo Santiago ALCM, Das K, Manimohan P, Gibertoni TB, Lim YW, Ekanayaka AH, Thongbai B, Lee HB, Yang JB, Kirk PM, Sysouphanthong P, Singh SK, Boonmee S, Dong W, Raj KNA, Latha KPD, Phookamsak R, Phukhamsakda C, Konta S, Jayasiri SC, Norphanphoun C, Tennakoon DS, Li JF, Dayarathne MC, Perera RH, Xiao YP, Wanasinghe DN, Senanayake IC, Goonasekara ID, de Silva NI, Mapook A, Jayawardena RS, Dissanayake AJ, Manawasinghe IS, Chethana KWT, Luo ZL, Hapuarachchi KK, Baghela A, Soares AM, Vizzini A, Meiras-Ottoni A, Mesic A, Dutta AK, de Souza CAF, Richter C, Lin CG, Chakrabarty D, Daranagama DA, Lima DX, Chakraborty D, Ercole E, Wu F, Simonini G, Vasquez G, Alves da Silva G, Plautz Jr HL, Ariyawansa HA, Lee H, Kušan I, Song J, Sun JZ, Karmakar J, Hu KF, Semwal KC, Thambugala KM, Voigt K, Acharya K, Rajeshkumar KC, Ryvarden L, Jadan M, Hosen MI, Mikšík M, Samarakoon MC, Wijayawardene NN, Kim NK, Matočec N, Singh PN, Tian Q, Bhatt RP, Vilela de Oliveira RJ, Tulloss RE, Aamir S, Kaewchai S, Marathe SD, Khan S, Hongsanan S, Adhikari S, Mehmood Bandyopadhyay TK, Svetasheva TY, Nguyen TTT, Vladimír Antonín V, Li WJ, Wang Y, Indoliya Y, Tkalčec Z, Elgorban AM, Bahkali AH, Tang AMC, Su HY, Zhang H, Promputtha I, Luangsa-ard J, Xu JC, Yan JY, Kang JC, Stadler M, Mortimer PE, Chomnunti P, Zhao Q, Phillips ALL, Nontachaiyapoom S, Wen TC, Karunarathna SC (2017) Fungal diversity notes 491–602: Taxonomic and phylogenetic contributions to fungal taxa. Fungal Diversity 43(1): 1–261. https://doi.org/10.1007/s13225-017-0378-0

Tibpromma S, Hyde KD, McKenzie EHC, Bhat DJ, Phillips AJL, Wanasinghe DN, Samarakoon MC, Jayawardena RS, Dissanayake AJ, Tennakoon DS, Doilom M, Phookamsak R, Tang

AMC, Xu JC, Mortimer PE, Promputtha I, Maharachchikumbura SSN, Khan S, Karunarathna SC (2018) Fungal diversity notes 840–928: Micro–fungi associated with Pandanaceae. Fungal Diversity 93(1): 1–60. https://doi.org/10.1007/s13225-018-0408-6

Tsui CKM, Khiang Goh T, Hyde KD, Hodgkiss IJ (2001) New species or records of *Cacumisporium*, *Helicosporium*, *Monotosporella* and *Bahusutrabeeja* on submerged wood in Hong Kong streams. Mycologia 93(2): 389–397. https://doi.org/10.1080/00275514.2001.12063170

Vaidya G, Lohman DJ, Meier R (2011) SequenceMatrix: Concatenation software for the fast assembly of multi-gene datasets with character set and codon information. Cladistics 27(2): 171–180. https://doi.org/10.1111/j.1096-0031.2010.00329.x

Vilgalys R, Hester M (1990) Rapid genetic identification and mapping of enzymatically amplified ribosomal DNA from several Cryptococcus species. Journal of Bacteriology 172: 4238–4246. https://doi.org/10.1128/jb.172.8.4238-4246.1990

Wanasinghe DN, Jeewon R, Jones EBG, Boonmee S, Kaewchai S, Manawasinghe IS, Lumyong S, Hyde KD (2018a) Novel palmicolous taxa within Pleosporales: Multigene phylogeny and taxonomic circumscription. Mycological Progress 17(5): 571–590. https://doi.org/10.1007/s11557-018-1379-4

Wanasinghe DN, Phukhamsakda C, Hyde KD, Jeewon R, Lee HB, Jones EBG, Tibpromma S, Tennakoon DS, Dissanayake AJ, Jayasiri SC, Gafforov Y, Camporesi E, Bulgakov TS, Ekanayake AH, Perera RH, Samarakoon MC, Goonasekara ID, Mapook A, Li WJ, Senanayake IC, Li JF, Norphanphoun C, Doilom M, Bahkali AH, Xu JC, Mortimer PE, Tibell L, Tibell S, Karunarathna SC (2018b) Fungal diversity notes 709–839: Taxonomic and phylogenetic contributions to fungal taxa with an emphasis on fungi on Rosaceae. Fungal Diversity 89(1): 1–236. https://doi.org/10.1007/s13225-018-0395-7

White TJ, Bruns T, Lee S, Taylor J (1990) Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In: Innis MA, Gelfand DH, Sninsky JJ, White TJ (Eds) PCR Protocols a Guide to Methods and Applications. Academic Press, New York, 315–322. https://doi.org/10.1016/B978-0-12-372180-8.50042-1

Whitton SR, McKenzie EHC, Hyde KD (2002) Microfungi on the Pandanaceae: Two new species of *Camposporium* and key to the genus. Fungal Diversity 11: 177–187.

Wijayawardene NN, Crous PW, Kirk PM, Hawksworth DL, Boonmee S, Braun U, Dai DQ, D'souza MJ, Diederich P, Dissanayake A, Doilom M, Hongsanan S, Jones EBG, Groenewald JZ, Jayawardena R, Lawrey JD, Liu JK, Lücking R, Madrid H, Manamgoda DS, Muggia L, Nelsen MP, Phookamsak R, Suetrong S, Tanaka K, Thambugala KM, Wanasinghe DN, Wikee S, Zhang Y, Aptroot A, Ariyawansa HA, Bahkali AH, Bhat JD, Gueidan C, Chomnunti P, Hoog GSD, Knudsen K, Li WJ, McKenzie EHC, Miller AN, Phillips AJL, Pistek M, Raja HA, Shivas RS, Slippers B, Taylor JE, Tian Q, Wang Y, Woudenberg JHC, Cai L, Jaklitsch WM, Hyde KD (2014a) Naming and outline of Dothideomycetes–2014 including proposals for the protection or suppression of generic names. Fungal Diversity 69(1): 1–55. https://doi.org/10.1007/s13225-014-0309-2

Wijayawardene NN, Hyde KD, Bhat DJ, Camporesi E, Schumacher RK, Chethana KWT, Wikee S, Bahkali AH, Wang Y (2014b) *Camarosporium*–like species are polyphyletic in Pleosporales; introducing *Paracamarosporium* and *Pseudocamarosporium* gen. nov. in Montagnulaceae. Cryptogamie. Mycologie 35(2): 177–198. https://doi.org/10.7872/crym.v35.iss2.2014.177

Wijayawardene NN, Hyde KD, Rajeshkumar KC, Hawksworth DL, Madrid H, Kirk PM, Braun U, Singh RV, Crous PW, Kukwa M, Lu¨cking R, Kurtzman CP, Yurkov A, Haelewaters D, Aptroot A, Lumbsch HT, Timdal E, Ertz D, Etayo J, Phillips AJL, Groenewald JZ, Papizadeh M, Selbmann L, Dayarathne MC, Weerakoon G, Jones EBG, Suetrong S, Tian

Q, Castan˜eda-Ruiz RF, Bahkali AH, Pang K-L, Tanaka K, Dai DQ, Sakayaroj J, Hujslova´ M, Lombard L, Shenoy BD, Suija A, Maharachchikumbura SSN, Thambugala KM, Wanasinghe DN, Sharma BO, Gaikwad S, Pandit G, Zucconi L, Onofri S, Egidi E, Raja HA, Kodsueb R, Ca'ceres MES, Pe'rez-Ortega S, Fiuza PO, Monteiro JS, Vasilyeva LN, Shivas RG, Prieto M, Wedin M, Olariaga I, Lateef AA, Agrawal Y, Fazeli SAS, Amoozegar MA, Zhao GZ, Pfliegler WP, Sharma G, Oset M, Abdel-Wahab MA, Takamatsu S, Bensch K, de Silva NI, De Kese A, Karunarathna A, Boonmee S, Pfister DH, Lu Y-Z, Luo Z-L, Boonyuen N, Daranagama DA, Senanayake IC, Jayasiri SC, Samarakoon MC, Zeng X-Y, Doilom M, Quijada L, Rampadarath S, Heredia G, Dissanayake AJ, Jayawardana RS, Perera RH, Tang LZ, Phukhamsakda C, Herna'ndez-Restrepo M, Ma X, Tibpromma S, Gusmao LFP, Weerahewa D, Karunarathna SC (2017) Notes for genera: Ascomycota. Fungal Diversity 86(1): 1–594. https://doi.org/10.1007/s13225-017-0386-0

Wijayawardene NN, Hyde KD, Al–ani LKT, Tedersoo L, Haelewaters D, Rajeshkumar KC, Zhao RL, Aptroot A, Leontyev DV, Ramesh K, Saxena RK, Tokarev YS, Dai DQ, Letcher PM, Stephenson SL, Ertz D, Lumbsch HT, Kukwa M, Issi IV, Madrid H, Phillips AJL, Selbmann L, Pfliegler WP, Horváth E, Bensch K, Kirk PM, Kolaříková K, Raja HA, Radek R, Papp V, Dima V, Ma J, Malosso E, Takamatsu S, Rambold G, Gannibal PB, Triebel D, Gautam AK, Avasthi S, Suetrong S, Timdal E, Fryar SC, Delgado G, Réblová M, Doilom M, Dolatabadi S, Pawłowska JZ, Humber RA, Kodsueb R (2020) Outline of Fungi and fungus–like taxa. Mycosphere 11(1): 1060–1456. https://doi.org/10.5943/mycosphere/11/1/8

Wijayawardene NN, Hyde KD, Dai DQ, Sánchez–García M, Goto BT, Saxena RK, Erdoğdu M, Selçuk F, Rajeshkumar KC, Aptroot A, Błaszkowski J, Boonyuen N, da Silva GA, de Souza FA, Dong W, Ertz D, Haelewaters D, Jones EBG, Karunarathna SC, Kirk PM, Kukwa M, Kumla J, Leontyev DV, Lumbsch HT, Maharachchikumbura SSN, Marguno F, Martínez-Rodríguez P, Mešić A, Monteiro JS, Oehl F, Pawłowska J, Pem D, Pfliegler WP, Phillips AJL, Pošta A, He MQ, Li JX, Raza M, Sruthi OP, Suetrong S, Suwannarach N, Tedersoo L, Thiyagaraja V, Tibpromma S, Tkalčec Z, Tokarev YS, Wanasinghe DN, Wijesundara DSA, Wimalaseana SDMK, Madrid H, Zhang GQ, Gao Y, Sánchez-Castro I, Tang LZ, Stadler M, Yurkov A, Thines M (2022) Outline of Fungi and fungus-like taxa – 2021. Mycosphere 13(1): 53–453. https://doi.org/10.5943/mycosphere/13/1/2

Winter GP (1885) Pilze–Ascomyceten. GL Rabenhorst's Kryptogamen–Flora von Deutschland, Oesterreich und der Schweiz 1: 65–528.

Yang J, Liu NG, Liu JK, Hyde KD, Jones EBG, Liu ZY (2018) Phylogenetic placement of *Cryptophiale*, *Cryptophialoidea*, *Nawawia*, *Neonawawia* gen. nov. and *Phialosporostilbe*. Mycosphere 9(6): 1132–1150. https://doi.org/10.5943/mycosphere/9/6/5

Yang J, Liu LL, Jones EBG, Li WL, Hyde KD, Liu ZY (2021) Morphological Variety in *Distoseptispora* and Introduction of Six Novel Species. Journal of Fungi 7(11): 945. https://doi.org/10.3390/jof7110945

Yang J, Liu LL, Jones EBG, Hyde KD, Liu ZY, Bao DF, Liu NG, Li WL, Shen HW, Yu XD, Liu JK (2023) Freshwater fungi from karst landscapes in China and Thailand. Fungal Diversity 119(1): 1–212. https://doi.org/10.1007/s13225-023-00514-7

Zhang H, Jones GEB, Zhou D, Bahkali AH, Hyde KD (2011) Checklist of freshwater fungi in Thailand. Cryptogamie. Mycologie 32(2): 199–217. https://doi.org/10.7872/crym.v32.iss2.2011.199

Zhang Y, Crous PW, Schoch CL, Hyde KD (2012) Pleosporales. Fungal Diversity 52(1): 1–225. https://doi.org/10.1007/s13225-011-0117-x

Zhang Y, Fournier J, Phookamsak R, Bahkali AH, Hyde KD (2013) Halotthiaceae fam. nov. (Pleosporales) accommodates the new genus *Phaeoseptum* and several other aquatic genera. Mycologia 105(3): 603–609. https://doi.org/10.3852/11-286